```
DEFINITION  HS_5142_A1_D07_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=718 Col=13 Row=G, DNA sequence.
ACCESSION   AQ457751
VERSION     AQ457751.1  GI:4636391
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 718  row: G  column: 13
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 454.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=718 Col=13 Row=G"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      128 a     83 c     95 g    145 t      3 others
ORIGIN


  Query Match             85.6%;  Score 15.4;  DB 97;  Length 454;
  Best Local Similarity   94.1%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ctcccagcgtgcgccat 18
           |||||||||| |||||
Db     300 CTCCCAGCGTGAGCCAT 316


Search completed: December  4, 2000, 21:06:39
Job time: 19239 sec
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```
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 456.
FEATURES              Location/Qualifiers
     source           1. .525
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2662007"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /lab_host="DH10B"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo. "
BASE COUNT      154 a    104 c    111 g    155 t      1 others
ORIGIN


  Query Match             88.9%;  Score 16;  DB 20;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tcccagcgtgcgccat 18
          ||||||||||||||||
Db    305 TCCCAGCGTGCGCCAT 320


RESULT  13
AI982970
LOCUS       AI982970      735 bp    mRNA            EST       31-AUG-1999
DEFINITION  wt46b05.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510481 3'
            similar to TR:O43326 O43326 HYPOTHETICAL 65.4 KD PROTEIN. ;, mRNA
            sequence.
ACCESSION   AI982970
VERSION     AI982970.1  GI:5810189
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 426.
FEATURES              Location/Qualifiers
     source           1. .735
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2510481"
                      /clone_lib="NCI_CGAP_Pan1"
                      /tissue_type="adenocarcinoma"
                      /lab_host="DH10B"
                      /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.72 kb. Life Technologies catalog #:
                      11548-013"
BASE COUNT      215 a    150 c    153 g    217 t
ORIGIN


  Query Match             88.9%;  Score 16;  DB 14;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tcccagcgtgcgccat 18
          ||||||||||||||||
Db    304 TCCCAGCGTGCGCCAT 319


RESULT  14
AQ214736
LOCUS       AQ214736      416 bp    DNA             GSS       18-SEP-1998
DEFINITION  HS_3250_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3250 Col=9 Row=L, DNA sequence.
ACCESSION   AQ214736
VERSION     AQ214736.1  GI:3625937
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 416)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3250  row: L  column: 9
            Class: BAC ends
            High quality sequence stop: 416.
FEATURES              Location/Qualifiers
     source           1. .416
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="Plate=3250 Col=9 Row=L"
                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
                      /sex="male"
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                      E-Coli DH10B"
BASE COUNT      120 a    123 c     72 g    100 t      1 others
ORIGIN


  Query Match             85.6%;  Score 15.4;  DB 90;  Length 416;
  Best Local Similarity   94.1%;  Pred. No. 8.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ctcccagcgtgcgccat 18
          || ||||||||||||||
Db    177 CTACCAGCGTGCGCCAT 193


RESULT  15
AQ457751
LOCUS       AQ457751      454 bp    DNA             GSS       23-APR-1999
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                    Soares and M. Fatima Bonaldo. "
BASE COUNT      121 a      85 c      95 g     137 t       1 others
ORIGIN


  Query Match             88.9%;  Score 16;  DB 19;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tcccagcgtgcgccat 18
          ||||||||||||||||
Db    306 TCCCAGCGTGCGCCAT 321


RESULT 10
AI005163
LOCUS       AI005163      459 bp    mRNA            EST       27-AUG-1998
DEFINITION  ou13c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1626156 3' similar to TR:Q99499 Q99499 DYNEIN-RELATED
            PROTEIN. ;, mRNA sequence.
ACCESSION   AI005163
VERSION     AI005163.1  GI:3214673
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 703   Std Error: 0.00
            Seq primer: primer name ambiguous
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1626156"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      128 a      83 c      96 g     152 t
ORIGIN


  Query Match             88.9%;  Score 16;  DB 7;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tcccagcgtgcgccat 18
          ||||||||||||||||
Db    350 TCCCAGCGTGCGCCAT 365


RESULT 11
AI682599
LOCUS       AI682599      510 bp    mRNA            EST       17-DEC-1999
DEFINITION  wc63e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323340 3'
            similar to TR:O43326 O43326 HYPOTHETICAL 65.4 KD PROTEIN. ;, mRNA
            sequence.
ACCESSION   AI682599
VERSION     AI682599.1  GI:4892781
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1483   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 360.
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2323340"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT      143 a      89 c     110 g     168 t
ORIGIN


  Query Match             88.9%;  Score 16;  DB 12;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tcccagcgtgcgccat 18
          ||||||||||||||||
Db    349 TCCCAGCGTGCGCCAT 364


RESULT 12
AW182837
LOCUS       AW182837      525 bp    mRNA            EST       18-NOV-1999
DEFINITION  xj64d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2662007 3' similar to TR:O43326 O43326 HYPOTHETICAL 65.4 KD
            PROTEIN. ;, mRNA sequence.
ACCESSION   AW182837
VERSION     AW182837.1  GI:6451297
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
```

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RESULT   7
AI108632
LOCUS       AI108632      658 bp    mRNA            EST       18-NOV-1998
DEFINITION  GH07838.5prime GH Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone GH07838 5prime, mRNA sequence.
ACCESSION   AI108632
VERSION     AI108632.1  GI:3477167
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
            ,P., Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Harvey, D.
            G. M. Rubin-Molecular and Cell Biology
            University of California Berkeley
            539 LSA, Berkeley, CA 94720-3200, USA
            Fax: 510 643 9947
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 78  row: D  column: 2
            High quality sequence stop: 520.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="GH07838"
                     /clone_lib="GH Drosophila melanogaster head pOT2"
                     /sex="male and female"
                     /dev_stage="adult"
                     /lab_host="DH5 - alpha"
                     /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2.  Plasmid cDNA library."
BASE COUNT      167 a    188 c    190 g    113 t
ORIGIN


  Query Match             91.1%;  Score 16.4;  DB 8;  Length 658;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tctcccagcgtgcgccat 18
           || |||||||||||||||
Db      80 TCGCCCAGCGTGCGCCAT 97


RESULT   8
AA990787
LOCUS       AA990787      695 bp    mRNA            EST       24-NOV-1998
DEFINITION  LD34664.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD34664 5prime, mRNA sequence.
ACCESSION   AA990787
VERSION     AA990787.1  GI:3177320
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 695)
  AUTHORS   Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
            ,P., Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Harvey, D.
            G. M. Rubin-Molecular and Cell Biology
            University of California Berkeley
            539 LSA, Berkeley, CA 94720-3200, USA
            Fax: 510 643 9947
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 346  row: F  column: 4
            High quality sequence stop: 543.
FEATURES             Location/Qualifiers
     source          1. .695
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="LD34664"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
BASE COUNT      178 a    201 c    206 g    110 t
ORIGIN


  Query Match             91.1%;  Score 16.4;  DB 7;  Length 695;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tctcccagcgtgcgccat 18
           || |||||||||||||||
Db      66 TCGCCCAGCGTGCGCCAT 83


RESULT   9
AW070294
LOCUS       AW070294      439 bp    mRNA            EST       13-OCT-1999
DEFINITION  xa06g11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2567588 3' similar to TR:O43326 O43326 HYPOTHETICAL 65.4 KD
            PROTEIN. ;, mRNA sequence.
ACCESSION   AW070294
VERSION     AW070294.1  GI:6025292
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2567588"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: NOT I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
```

```
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 1759   Std Error: 0.00
          Seq primer: mob.REGA+ET.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Homo sapiens"
                     /db_xref="GDB:1278322"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:361619"
                     /clone_lib="Soares retina N2b4HR"
                     /sex="male"
                     /tissue_type="retina"
                     /dev_stage="55 year old"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). The retinas were obtained from a 55 year old
                     Caucasian  and total cellular poly(A)+ RNA was extracted 6
                     hrs after their removal. The retina RNA  was kindly
                     provided by Roderick R. McInnes M.D. Ph.D. from the
                     University  of Toronto. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. "
BASE COUNT       96 a    126 c    119 g     99 t      2 others
ORIGIN


  Query Match             91.1%;  Score 16.4;  DB 40;  Length 442;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          |||||||||||| |||||
Db    323 TCTCCCAGCGTGGGCCAT 306


RESULT   5
AI514786
LOCUS       AI514786      577 bp    mRNA            EST       16-MAR-1999
DEFINITION  LD46473.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD46473 5prime, mRNA sequence.
ACCESSION   AI514786
VERSION     AI514786.1  GI:4422958
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
            ,P., Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Harvey, D.
            G. M. Rubin-Molecular and Cell Biology
            University of California Berkeley
            539 LSA, Berkeley, CA 94720-3200, USA
            Fax: 510 643 9947
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 464  row: G  column: 1
            High quality sequence stop: 458.
FEATURES             Location/Qualifiers
     source          1. .577
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="LD46473"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
BASE COUNT      140 a    175 c    170 g     92 t
ORIGIN


  Query Match             91.1%;  Score 16.4;  DB 11;  Length 577;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          || ||||||||||||||||
Db     73 TCGCCCAGCGTGCGCCAT 90


RESULT   6
AI512315
LOCUS       AI512315      636 bp    mRNA            EST       16-MAR-1999
DEFINITION  LD44124.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD44124 5prime, mRNA sequence.
ACCESSION   AI512315
VERSION     AI512315.1  GI:4421733
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
            ,P., Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Harvey, D.
            G. M. Rubin-Molecular and Cell Biology
            University of California Berkeley
            539 LSA, Berkeley, CA 94720-3200, USA
            Fax: 510 643 9947
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 441  row: B  column: 12
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .636
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="LD44124"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
BASE COUNT      158 a    188 c    184 g    106 t
ORIGIN


  Query Match             91.1%;  Score 16.4;  DB 11;  Length 636;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          || ||||||||||||||||
Db     77 TCGCCCAGCGTGCGCCAT 94
```

```
VERSION     H83468.1  GI:1062139
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 398)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 305
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1825   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 305.
FEATURES             Location/Qualifiers
     source          1. .398
                     /organism="Homo sapiens"
                     /db_xref="GDB:3850898"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:222137"
                     /clone_lib="Soares retina N2b5HR"
                     /sex="male"
                     /tissue_type="retina"
                     /dev_stage="55 year old"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). The retinas were obtained from a 55 year old
                     Caucasian  and total cellular poly(A)+ RNA was extracted 6
                     hrs after their removal. The retina RNA  was kindly
                     provided by Roderick R. McInnes M.D. Ph.D. from the
                     University  of Toronto. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. "
BASE COUNT       85 a    104 c    108 g     98 t      3 others
ORIGIN
```

```
  Query Match             91.1%;  Score 16.4;  DB 37;  Length 398;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tctcccagcgtgcgccat 18
           ||||||||||||| ||||||
Db     324 TCTCCCAGCGTGGGCCAT 307
```

```
RESULT   3
AA402089
LOCUS       AA402089      412 bp    mRNA            EST       16-MAY-1997
DEFINITION  zu53f02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:741723 5' similar to SW:YK18_YEAST P36132 HYPOTHETICAL 46.6
            KD PROTEIN IN DAL80-GAP1 INTERGENIC REGION. ;, mRNA sequence.
ACCESSION   AA402089
VERSION     AA402089.1  GI:2056072
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 378.
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Homo sapiens"
                     /db_xref="GDB:5941912"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:741723"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT       77 a    115 c    131 g     89 t
ORIGIN
```

```
  Query Match             91.1%;  Score 16.4;  DB 4;  Length 412;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tctcccagcgtgcgccat 18
           ||||||||||||| ||||||
Db      77 TCTCCCAGCGTCCGCCAT 94
```

```
RESULT   4
W96258/c
LOCUS       W96258        442 bp    mRNA            EST       29-NOV-1996
DEFINITION  ze42b06.r1 Soares retina N2b4HR Homo sapiens cDNA clone
            IMAGE:361619 5', mRNA sequence.
ACCESSION   W96258
VERSION     W96258.1  GI:1426165
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
```

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16.4	91.1	387	37	H85916	H85916 ys95c07.r1
c	2	16.4	91.1	398	37	H83468	H83468 ys91b09.r1
	3	16.4	91.1	412	4	AA402089	AA402089 zu53f02.r
c	4	16.4	91.1	442	40	W96258	W96258 ze42b06.r1
	5	16.4	91.1	577	11	AI514786	AI514786 LD46473.5
	6	16.4	91.1	636	11	AI512315	AI512315 LD44124.5
	7	16.4	91.1	658	8	AI108632	AI108632 GH07838.5
	8	16.4	91.1	695	7	AA990787	AA990787 LD34664.5
	9	16	88.9	439	19	AW070294	AW070294 xa06g11.x
	10	16	88.9	459	7	AI005163	AI005163 ou13c07.x
	11	16	88.9	510	12	AI682599	AI682599 wc63e11.x
	12	16	88.9	525	20	AW182837	AW182837 xj64d12.x
	13	16	88.9	735	14	AI982970	AI982970 wt46b05.x
	14	15.4	85.6	416	90	AQ214736	AQ214736 HS_3250_B
	15	15.4	85.6	454	97	AQ457751	AQ457751 HS_5142_A
c	16	15.4	85.6	467	100	AQ649394	AQ649394 Sheared D
c	17	15.4	85.6	601	115	FR0021601	AL014474 F.rubripe
c	18	15.4	85.6	686	100	AQ655156	AQ655156 Sheared D
c	19	15.4	85.6	783	113	CNS01T6S	AL166141 Tetraodon
c	20	15.4	85.6	1027	114	CNS04CRA	AL284815 Tetraodon
c	21	15	83.3	231	5	AA625067	AA625067 af66g07.r
	22	15	83.3	719	114	CNS049ZN	AL281228 Tetraodon
c	23	15	83.3	871	36	BE545551	BE545551 601070216
c	24	14.8	82.2	168	108	AZ208425	AZ208425 SP_0150_A
	25	14.8	82.2	185	4	AA421434	AA421434 zu27g02.r
c	26	14.8	82.2	191	103	AQ843749	AQ843749 LMAJFV1_1
	27	14.8	82.2	224	6	AA853590	AA853590 NHTBCae06
c	28	14.8	82.2	246	20	AW183217	AW183217 xj74a08.x
	29	14.8	82.2	254	16	AV134225	AV134225 AV134225
c	30	14.8	82.2	310	104	AQ911626	AQ911626 LMAJFV1_1
	31	14.8	82.2	346	4	AA465312	AA465312 aa24b11.r
	32	14.8	82.2	363	106	AZ043716	AZ043716 RPCI-23-3
c	33	14.8	82.2	380	103	AQ843748	AQ843748 LMAJFV1_1
c	34	14.8	82.2	413	32	BE008986	BE008986 CM4-BN016
	35	14.8	82.2	413	33	BE119385	BE119385 UI-R-CA0-
	36	14.8	82.2	426	3	AA364148	AA364148 EST74711
c	37	14.8	82.2	428	14	AL040548	AL040548 DKFZp434I
	38	14.8	82.2	437	115	FR0008579	Z92389 F.rubripes
	39	14.8	82.2	442	21	AW246200	AW246200 2821849.5
	40	14.8	82.2	443	34	BE255160	BE255160 601113191
	41	14.8	82.2	467	34	BE264833	BE264833 601194308
	42	14.8	82.2	475	38	N28555	N28555 yx37f03.r1
	43	14.8	82.2	487	5	AA605873	AA605873 fa20g10.s
c	44	14.8	82.2	511	24	AW719286	AW719286 LjNEST_C1
	45	14.8	82.2	522	98	AQ502968	AQ502968 V47D5 mTn

ALIGNMENTS

RESULT 1
H85916/c

LOCUS H85916 387 bp mRNA EST 21-NOV-1995
DEFINITION ys95c07.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222540 5', mRNA sequence.
ACCESSION H85916
VERSION H85916.1 GI:1067495
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 387)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 305
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1370 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 305.
FEATURES Location/Qualifiers
source 1. .387
/organism="Homo sapiens"
/db_xref="GDB:3851301"
/db_xref="taxon:9606"
/clone="IMAGE:222540"
/clone_lib="Soares retina N2b5HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
BASE COUNT 82 a 100 c 107 g 95 t 3 others
ORIGIN

Query Match 91.1%; Score 16.4; DB 37; Length 387;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctcccagcgtgcgccat 18
||||||||||||| |||||
Db 327 TCTCCCAGCGTGGGCCAT 310

RESULT 2
H83468/c
LOCUS H83468 398 bp mRNA EST 13-NOV-1995
DEFINITION ys91b09.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222137 5', mRNA sequence.
ACCESSION H83468

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 15:46:00 ; Search time 1141.84 Seconds
(without alignments)
97.466 Million cell updates/sec

Title: US-09-369-941-1
Perfect score: 18
Sequence: 1 tctcccagcgtgcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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8: gb_est8:*
9: gb_est9:*
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11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
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101: gb_gss10:*
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111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 15:46:00 ; Search time 993.06 Seconds
(without alignments)
79.166 Million cell updates/sec

Title: US-09-369-941-1
Perfect score: 18
Sequence: 1 tctcccagcgtgcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: gb_ba3:*
31: gb_in1:*
32: gb_in2:*
33: gb_in3:*
34: gb_pl3:*
35: gb_pr4:*
36: em_ba1:*
37: em_ba2:*
38: em_htg1:*
39: em_htg2:*
40: em_htg3:*
41: em_htg4:*
42: em_htg5:*
43: em_htg6:*
44: em_htg7:*
45: em_htg8:*
46: em_htg9:*
47: em_htg10:*
48: em_htg11:*
49: em_htg12:*
50: em_htg13:*
51: em_htg14:*
52: em_htg15:*
53: em_htg16:*
54: em_htg17:*
55: em_htg18:*
56: em_htg19:*
57: em_htg20:*
58: em_htg21:*
59: em_htg22:*
60: em_htg23:*
61: em_hum3:*
62: em_hum4:*
63: em_hum5:*
64: em_hum6:*
65: gb_pr5:*
66: gb_pr6:*
67: gb_pr7:*
68: gb_htg1:*
69: gb_htg2:*
70: gb_htg3:*
71: gb_htg4:*
72: gb_htg5:*
73: gb_htg6:*
74: gb_htg7:*
75: gb_htg8:*
76: gb_htg9:*
77: gb_htg10:*
78: gb_htg11:*
79: gb_htg12:*
80: gb_htg13:*
81: gb_htg14:*
82: gb_htg15:*
83: gb_htg16:*
84: gb_htg17:*
85: gb_htg18:*
86: gb_htg19:*
87: gb_htg20:*
88: gb_htg21:*
89: gb_htg22:*
90: gb_htg23:*
91: gb_sts1:*
92: gb_sts2:*
93: gb_vi1:*
94: gb_vi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		18	100.0	18	5	AR052619	AR052619 Sequence
2		18	100.0	18	5	AR052624	AR052624 Sequence
3		18	100.0	18	5	I96098	I96098 Sequence 17
c 4		18	100.0	27	5	AR004426	AR004426 Sequence
c 5		18	100.0	27	5	I43661	I43661 Sequence 13
c 6		18	100.0	27	5	I86720	I86720 Sequence 8
c 7		18	100.0	35	5	AR052604	AR052604 Sequence
c 8		18	100.0	35	5	I96083	I96083 Sequence 2
c 9		18	100.0	454	67	S72602	S72602 bcl2 [human
c 10		18	100.0	615	5	AR052623	AR052623 Sequence
c 11		18	100.0	717	5	AR052622	AR052622 Sequence
c 12		18	100.0	760	5	AR021160	AR021160 Sequence

c	13	18	100.0	765	5	A76121
c	14	18	100.0	911	67	HUMBCL2B
c	15	18	100.0	1846	5	AR054009
c	16	18	100.0	1846	66	HSBCL2IG
c	17	18	100.0	5086	5	AR052621
c	18	18	100.0	5086	5	AR054008
c	19	18	100.0	5086	67	HUMBCL2A
c	20	18	100.0	5105	5	I08038
c	21	18	100.0	6030	67	HUMBCL2C
c	22	18	100.0	86692	75	AC021803
	23	18	100.0	169542	89	AP001915
	24	18	100.0	188601	69	AC009267
	25	17	94.4	17	5	I96090
	26	17	94.4	35737	9	AC005263
c	27	16.4	91.1	67568	74	AC020378
c	28	16.4	91.1	99614	68	AC008358
c	29	16.4	91.1	128132	68	AC007732
c	30	16.4	91.1	161799	9	AC002091
	31	16.4	91.1	170757	68	AC007608
c	32	16.4	91.1	186323	68	AC006491
c	33	16.4	91.1	210299	31	AE003690
	34	16.4	91.1	217026	72	AC013669
	35	16	88.9	157432	83	AC069438
	36	16	88.9	158934	81	AC055780
	37	16	88.9	211341	85	AL138898
c	38	15.4	85.6	10854	1	AE001886
c	39	15.4	85.6	38616	9	AC004208
c	40	15.4	85.6	42245	9	AC004476
	41	15.4	85.6	75163	83	AC069103
	42	15.4	85.6	75533	68	AC006412
	43	15.4	85.6	112630	78	AC025461
	44	15.4	85.6	117143	67	HUMBRCA1
	45	15.4	85.6	120841	10	AC008162

A76121 Sequence 1
M13995 Human B-cel
AR054009 Sequence
X06487 H.sapiens m
AR052621 Sequence
AR054008 Sequence
M13994 Human B-cel
I08038 Sequence 1
M14745 Human bcl-2
AC021803 Homo sapi
AP001915 Homo sapi
AC009267 Homo sapi
I96090 Sequence 9
AC005263 Homo sapi
AC020378 Drosophil
AC008358 Drosophil
AC007732 Homo sapi
AC002091 Genomic s
AC007608 Homo sapi
AC006491 Drosophil
AE003690 Drosophil
AC013669 Homo sapi
AC069438 Homo sapi
AC055780 Homo sapi
AL138898 Homo sapi
AE001886 Deinococc
AC004208 Homo sapi
AC004476 Homo sapi
AC069103 Homo sapi
AC006412 Homo sapi
AC025461 Homo sapi
L78833 Human BRCA1
AC008162 Homo sapi

ALIGNMENTS

```
RESULT   1
AR052619
LOCUS       AR052619        18 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 17 from patent US 5831066.
ACCESSION   AR052619
VERSION     AR052619.1  GI:5975983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 17 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      4 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   2
AR052624
LOCUS       AR052624        18 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 24 from patent US 5831066.
ACCESSION   AR052624
VERSION     AR052624.1  GI:5975988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 24 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   3
I96098
LOCUS       I96098          18 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 17 from patent US 5734033.
ACCESSION   I96098
VERSION     I96098.1  GI:3940568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 17 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      8 c      4 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   4
AR004426/c
LOCUS       AR004426        27 bp    DNA             PAT       04-DEC-1998
DEFINITION  Sequence 13 from patent US 5747245.
ACCESSION   AR004426
VERSION     AR004426.1  GI:3965305
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Reed,J.C. and Sato,T.
  TITLE     Nucleic acids encoding Fas associated proteins and screening assays
            using same
  JOURNAL   Patent: US 5747245-A 13 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
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```
BASE COUNT        7 a      6 c     10 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT   5
I43661/c
LOCUS       I43661         27 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 13 from patent US 5632994.
ACCESSION   I43661
VERSION     I43661.1  GI:2468759
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Reed,J.C. and Sato,T.
  TITLE     Fas associated proteins
  JOURNAL   Patent: US 5632994-A 13 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      6 c     10 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT   6
I86720/c
LOCUS       I86720         27 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 8 from patent US 5702897.
ACCESSION   I86720
VERSION     I86720.1  GI:3206438
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Reed,J.C. and Sato,T.
  TITLE     Interaction of proteins involved in a cell death pathway
  JOURNAL   Patent: US 5702897-A 8 30-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      6 c     10 g      4 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT   7
AR052604/c
LOCUS       AR052604       35 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 2 from patent US 5831066.
ACCESSION   AR052604
VERSION     AR052604.1  GI:5975968
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 2 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        6 a      8 c     13 g      8 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     35 TCTCCCAGCGTGCGCCAT 18


RESULT   8
I96083/c
LOCUS       I96083         35 bp    DNA             PAT       01-DEC-1998
DEFINITION  Sequence 2 from patent US 5734033.
ACCESSION   I96083
VERSION     I96083.1  GI:3940553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Reed,J.
  TITLE     Antisense oligonucleotides inhibiting human bcl-2 gene expression
  JOURNAL   Patent: US 5734033-A 2 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        6 a      8 c     13 g      8 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     35 TCTCCCAGCGTGCGCCAT 18


RESULT   9
S72602/c
LOCUS       S72602         454 bp    DNA             PRI       07-MAY-1993
DEFINITION  bcl2 [human, 697 pre-B cell acute lymphocytic leukemia cell line,
            Genomic, 454 nt].
ACCESSION   S72602
VERSION     S72602.1  GI:241046
KEYWORDS    .
SOURCE      human 697 pre-B cell acute lymphocytic leukemia cell line.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
```

```
  AUTHORS   Tanaka,S., Louie,D.C., Kant,J.A. and Reed,J.C.
  TITLE     Frequent incidence of somatic mutations in translocated BCL2
            oncogenes of non-Hodgkin's lymphomas
  JOURNAL   Blood 79 (1), 229-237 (1992)
  MEDLINE   92096610
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 72602] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .454
                     /partial
                     /gene="bcl2"
     CDS             41. .433
                     /partial
                     /gene="bcl2"
                     /note="Unknown"
                     /codon_start=1
                     /protein_id="AAD14111.1"
                     /db_xref="GI:4261811"
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFA"
BASE COUNT       65 a    170 c    150 g     69 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 67;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     58 TCTCCCAGCGTGCGCCAT 41


RESULT  10
AR052623/c
LOCUS       AR052623      615 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 22 from patent US 5831066.
ACCESSION   AR052623
VERSION     AR052623.1  GI:5975987
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 22 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .615
                     /organism="unknown"
BASE COUNT       98 a    203 c    213 g    101 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 615;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     18 TCTCCCAGCGTGCGCCAT 1


RESULT  11
AR052622/c
LOCUS       AR052622      717 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 20 from patent US 5831066.
ACCESSION   AR052622
VERSION     AR052622.1  GI:5975986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 20 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="unknown"
BASE COUNT      113 a    237 c    237 g    130 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 717;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     18 TCTCCCAGCGTGCGCCAT 1


RESULT  12
AR021160/c
LOCUS       AR021160      760 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 11 from patent US 5789389.
ACCESSION   AR021160
VERSION     AR021160.1  GI:3975775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   Tarasewicz,D.G., Schott,B., Holzmayer,T.A. and Roninson,I.B.
  TITLE     BCL2 derived genetic elements associated with sensitivity to
            chemotherapeutic drugs
  JOURNAL   Patent: US 5789389-A 11 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .760
                     /organism="unknown"
BASE COUNT      122 a    250 c    246 g    142 t
ORIGIN


  Query Match             100.0%;  Score 18;  DB 5;  Length 760;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     38 TCTCCCAGCGTGCGCCAT 21


RESULT  13
A76121/c
LOCUS       A76121        765 bp    DNA             PAT       19-OCT-1999
DEFINITION  Sequence 1 from Patent WO9320200.
ACCESSION   A76121
VERSION     A76121.1  GI:6088257
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   Evan,G.I.
  TITLE     MODIFIED CELLS AND METHOD OF TREATMENT
  JOURNAL   Patent: WO 9320200-A 14-OCT-1993;
            IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
FEATURES             Location/Qualifiers
     source          1. .765
```

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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="18"
     CDS             31. .750
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAB58588.1"
                     /db_xref="GI:6088258"
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVE
                     SVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLK
                     TLLSLALVGACITLGAYLSHK"
BASE COUNT      120 a    251 c    250 g    144 t
ORIGIN
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Query Match 100.0%; Score 18; DB 5; Length 765;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tctcccagcgtgcgccat 18
           ||||||||||||||||||
Db      48 TCTCCCAGCGTGCGCCAT 31
```

```
RESULT  14
HUMBCL2B/c
LOCUS       HUMBCL2B      911 bp    mRNA            PRI       31-OCT-1994
DEFINITION  Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
            encoding bcl-2-beta protein, complete cds.
ACCESSION   M13995
VERSION     M13995.1  GI:179368
KEYWORDS    alternative splicing; bcl-2-beta protein; proto-oncogene.
SOURCE      Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones
            B[15,16]; and DNA, clone lambda-18-27.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Tsujimoto,Y. and Croce,C.M.
  TITLE     Analysis of the structure, transcripts, and protein products of
            bcl-2, the gene involved in human follicular lymphoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
  MEDLINE   86259760
COMMENT     Clean copy sequence for [1] kindly provided by Y.Tsujimoto,
            10-FEB-1987.  The bcl-2 gene is transcribed by alternative splicing
            into three mRNAs of different sizes.  It consists of at least two
            exons and encodes two proteins which only differ at their
            carboxy-terminal ends, and it is activated by translocation into
            poximity with the Ig heavy chain locus.  Both the normal and
            rearranged bcl-2 gene products are expressed in the B-cell
            leukemia/lymphoma 2 cells.  Genomic clone lambda-18-27 contained
            all the DNA sequences on the 5' of the splice site (position 732).
FEATURES             Location/Qualifiers
     source          1. .911
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="18q21.3"
     mRNA            <1. .>911
                     /note="bcl2a mRNA"
     gene            147. .764
                     /gene="BCL2"
     CDS             147. .764
                     /gene="BCL2"
                     /note="bcl2-beta protein"
                     /codon_start=1
                     /db_xref="GDB:G00-119-031"
                     /protein_id="AAA51814.1"
                     /db_xref="GI:179369"
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVE
                     SVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWVGASGDVSLG"
     misc_feature    732
                     /gene="BCL2"
                     /note="alternative splice donor (intron A start)"
BASE COUNT      156 a    281 c    306 g    168 t
ORIGIN      556 bp upstream of SstI site.
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Query Match 100.0%; Score 18; DB 67; Length 911;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 tctcccagcgtgcgccat 18
           ||||||||||||||||||
Db     164 TCTCCCAGCGTGCGCCAT 147
```

```
RESULT  15
AR054009/c
LOCUS       AR054009      1846 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 16 from patent US 5834306.
ACCESSION   AR054009
VERSION     AR054009.1  GI:5978871
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1846)
  AUTHORS   Webster,K.A. and Bishopric,N.H.
  TITLE     Tissue specific hypoxia regulated therapeutic constructs
  JOURNAL   Patent: US 5834306-A 16 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1846
                     /organism="unknown"
BASE COUNT      424 a    520 c    483 g    419 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tctcccagcgtgcgccat 18
           ||||||||||||||||||
Db     904 TCTCCCAGCGTGCGCCAT 887
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Search completed: December 4, 2000, 20:47:25
Job time: 18085 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 16:32:02 ; Search time 99.31 Seconds
(without alignments)
68.089 Million cell updates/sec

Title: US-09-369-941-1
Perfect score: 18
Sequence: 1 tctcccagcgtgcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	16	Q86659	Bcl-2 antisense ol
2	18	100.0	18	19	V52545	Unmethylated CpG d
3	18	100.0	18	19	V27719	Immunostimulatory
4	18	100.0	18	19	V28181	Antisense oligonuc
5	18	100.0	18	19	V19667	Human bcl-2 antise
6	18	100.0	18	20	Z31944	CpG adjuvant oligo
7	18	100.0	18	20	Z41905	IL-12 secretion in
8	18	100.0	18	20	Z41948	IL-12 secretion in
9	18	100.0	18	20	X78803	HPV fusion protein
10	18	100.0	18	20	X88537	Cytosine-guanosine
11	18	100.0	18	20	X33514	BCL2-targeted anti
12	18	100.0	18	20	X23693	Deletion sequence
c 13	18	100.0	18	20	X27536	Synthetic RNA sequ
14	18	100.0	18	20	X18702	Target bcl-2 antis
15	18	100.0	18	20	V99434	Antisense oligonuc
16	18	100.0	18	21	Z99003	CpG motif for immu
17	18	100.0	18	21	Z60975	Nucleotide sequenc
18	18	100.0	18	21	Z87997	BBTE-labeled oligo
19	18	100.0	18	21	Z98660	Human Bcl-2 therap
20	18	100.0	18	21	Z47643	Parasitic infectio
21	18	100.0	18	21	Z47680	Parasitic infectio
22	18	100.0	18	21	Z47850	Immunostimulatory
23	18	100.0	18	21	Z47981	Immune remodeling
24	18	100.0	18	21	Z48024	Immune remodeling
25	18	100.0	20	20	V74246	CpG-N motif SOS-OD
c 26	18	100.0	27	17	T18388	Human Bcl-2 forwar
c 27	18	100.0	35	16	Q86644	Bcl-2 translation
c 28	18	100.0	35	19	V19652	Human bcl-2 oligon
c 29	18	100.0	251	19	X11646	Human biallelic po
c 30	18	100.0	251	19	X12817	Human biallelic po
c 31	18	100.0	615	16	Q73987	Human bcl-2 gene O
c 32	18	100.0	760	17	T33694	Human BCL2 cDNA.
c 33	18	100.0	765	14	Q49815	Bcl-2. Homo sapie
c 34	18	100.0	831	9	N81293	Sequence of bcl-2
c 35	18	100.0	911	20	X08431	bcl-2 proto-oncoge
c 36	18	100.0	953	20	X33183	Bcl-2 DNA fragment
c 37	18	100.0	5086	15	Q54631	Human oncogene bcl
c 38	18	100.0	5086	16	Q86661	Human bcl-2 gene.
c 39	18	100.0	5086	19	X75766	Human bcl2 proto-o
c 40	18	100.0	5105	9	N81292	Sequence of bcl-2
c 41	18	100.0	7996	20	X33184	Base sequence of t
42	17	94.4	17	19	V19659	Human bcl-2 antise
43	16.4	91.1	18	19	V52559	Unmethylated CpG d
44	16.4	91.1	18	19	V47681	Unmethylated CpG d
45	16.4	91.1	18	19	V27733	Immunostimulatory

ALIGNMENTS

RESULT 1
Q86659
ID Q86659 standard; DNA; 18 BP.
XX
AC Q86659;
XX
DT 27-SEP-1995 (first entry)
XX
DE Bcl-2 antisense oligonucleotide.
XX
KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW chemoresistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..18
FT /*tag= a
FT /note= "3'-5' (antisense) sequence"
XX
PN WO9508350-A.
XX
PD 30-MAR-1995.
XX
PF 20-SEP-1994; 94WO-US10725.
XX
PR 20-SEP-1993; 93US-0124256.
XX
PA (REED/) REED J C.
XX
PI Reed JC;
XX
DR WPI; 1995-139394/18.
XX
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer
XX
PS Example 18; Page 44; 108pp; English.
XX
CC Reversal of chemoresistance of tumor cells by antisense-mediated
CC reduction of bcl1-2 expression was demonstrated using the
CC oligonucleotide given in Q86659. This is antisense to the first
CC 6 codons of the bcl-2 ORF.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcccagcgtgcgccat 18
||||||||||||||||||
Db 1 tctcccagcgtgcgccat 18

RESULT 2
V52545
ID V52545 standard; DNA; 18 BP.
XX
AC V52545;
XX
DT 20-NOV-1998 (first entry)
XX
DE Unmethylated CpG dinucleotide 1758.
XX
KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.
XX
OS Synthetic.
XX
PN WO9837919-A1.
XX
PD 03-SEP-1998.
XX
PF 25-FEB-1998; 98WO-US03678.
XX
PR 28-FEB-1997; 97US-0039405.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Schwartz DA;
XX
DR WPI; 1998-480941/41.
XX
PT Use of nucleic acids containing an unmethylated CpG - for treating a
PT subject having or at risk of having an acute decrement in air flow
PT or inhibiting an inflammatory response
XX
PS Example 4; Page 35; 65pp; English.
XX
CC This sequence represents an unmethylated CpG dinucleotide, and can be
CC used in the method of the invention. The method is for treating a subject
CC having, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with
CC Gram-positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcccagcgtgcgccat 18
||||||||||||||||||
Db 1 tctcccagcgtgcgccat 18

RESULT 3
V27719
ID V27719 standard; DNA; 18 BP.
XX
AC V27719;
XX
DT 01-OCT-1998 (first entry)
XX
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
PN WO9818810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19791.
XX
PR 30-OCT-1996; 96US-0738652.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Kline JN, Krieg AM;
XX
DR WPI; 1998-272127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at
PT least one unmethylated CpG dinucleotide, used for treating e.g.
PT tumours, infections or autoimmune disease
XX
PS Disclosure; Page 49; 109pp; English.
XX
CC V27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC of the invention. The ODNs contain at least one unmethylated CpG
CC dinucleotide, and have the formula:
CC 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
CC CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is
CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
CC does not contain a CCGG tetramer or more than one CCG or CGG trimer OR
CC 5' NX1X2CGX3X4N 3', where at least one nucleotide separates consecutive
CC CpGs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA, X3and X4
CC are selected from TpT or CpT, N is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCGG tetramer
CC or more than one CCG or CGG trimer.
CC The ODNs activate lymphocytes in a subject and redirect a subject's
CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells and
CC other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune diseases, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a
CC human.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

```
  Query Match             100.0%;  Score 18;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT   4
V28181
ID   V28181 standard; DNA; 18 BP.
XX
AC   V28181;
XX
DT   08-OCT-1998  (first entry)
XX
DE   Antisense oligonucleotide to bcl-2 mRNA.
XX
KW   Purification; oligonucleotide; matrix; affinity unit;
KW   affinity purification; antisense; bcl-2; ss.
XX
OS   Synthetic.
XX
PN   WO9827425-A1.
XX
PD   25-JUN-1998.
XX
PF   18-DEC-1997;   97WO-US23284.
XX
PR   19-DEC-1996;   96US-0769951.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Cole DL,  Srivatsa GS;
XX
DR   WPI; 1998-362922/31.
XX
PT   Matrix for selective separation of oligo:nucleotide - useful for,
PT   e.g. large scale purification of anti-sense agents from their
PT   deletion derivatives formed during synthesis
XX
PS   Disclosure; Page 86; 183pp; English.
XX
CC   V28155-268 represent oligonucleotides which can be purified using the
CC   method of the invention. The specification describes a matrix that
CC   comprises a support and an affinity unit that specifically and reversibly
CC   binds a target oligonucleotide, and comprises a sequence of bases having
CC   the reverse complement of a hybridising portion of the target
CC   oligonucleotide. The matrix is used for affinity purification of
CC   synthetic oligonucleotides, specifically antisense agents, for treatment
CC   of hyperproliferative diseases, for treating a non-pathogen,
CC   non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC   expression of cell surface proteins, and to inhibit a eukaryotic
CC   pathogen, retrovirus or other viruses.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT   5
V19667
ID   V19667 standard; DNA; 18 BP.
XX
AC   V19667;
XX
DT   12-JUN-1998  (first entry)
XX
DE   Human bcl-2 antisense oligonucleotide 13.
XX
KW   Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW   cancer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5734033-A.
XX
PD   31-MAR-1998.
XX
PF   24-MAR-1994;   94US-0288692.
XX
PR   21-FEB-1992;   92US-0840716.
PR   22-DEC-1988;   88US-0288692.
PR   24-MAR-1994;   94US-0217082.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Reed J;
XX
DR   WPI; 1998-229881/20.
XX
PT   Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT   for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
PS   Disclosure; Column 23; 21pp; English.
XX
CC   This antisense oligonucleotide is complementary to the translation
CC   initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
CC   oligonucleotides are phosphorothioate derivatives and can straddle
CC   strategic sites such as the translation initiation site, donor and
CC   acceptor splicing sites, or sites for transportation or degradation.
CC   Blocking translation at such strategic sites prevents the formation of
CC   a functional bcl-2 gene product. These oligonucleotides may be used for
CC   treating cancers associated with high levels of bcl-2 gene expression,
CC   especially lymphomas and some leukaemias.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT   6
Z31944
ID   Z31944 standard; DNA; 18 BP.
XX
AC   Z31944;
XX
DT   26-JAN-2000  (first entry)
XX
DE   CpG adjuvant oligo 1002.
XX
KW   CpG adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
KW   antigen; infection; allergy; cancer; therapy; ss.
XX
OS   Synthetic.
XX
PN   WO9952549-A1.
XX
```

PD 21-OCT-1999.
XX
PF 29-MAR-1999; 99WO-EP02278.
XX
PR 09-APR-1998; 98GB-0007805.
PR 25-SEP-1998; 98GB-0020956.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Friede M, Hermand P;
XX
DR WPI; 1999-620290/53.
XX
PT Vaccine to protect against infections, allergy and cancer -
XX
PS Example 9; Page 26; 52pp; English.
XX
CC This sequence represents a CpG adjuvant that can be used in the vaccine
CC composition of the invention. The vaccine comprises a polyoxyethylene
CC ether or ester (I), not in the form of a vesicle, pharmaceutically
CC acceptable excipient and an antigen (Ag) or antigenic composition. The
CC vaccine can be used to treat or prevent infections (by bacteria, viruses
CC or other parasites), allergy and cancer. (I), which are safe, easy to
CC sterilize and simple to administer, are powerful vaccine adjuvants, able
CC to induce a systemic immune response when administered (non-invasively)
CC to the mucosa. The response is at least as good as that from conventional
CC systemic injection. (I) are effective at low concentration, have low
CC reactogenicity and are well tolerated.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcccagcgtgcgccat 18
||||||||||||||||||
Db 1 tctcccagcgtgcgccat 18

RESULT 7
Z41905
ID Z41905 standard; DNA; 18 BP.
XX
AC Z41905;
XX
DT 24-JAN-2000 (first entry)
XX
DE IL-12 secretion inducing CpG oligonucleotide 50.
XX
KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW antigen presenting cell; infection; allergic disease.
XX
OS Synthetic.
XX
PN WO9951259-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07335.
XX
PR 03-APR-1998; 98US-0080729.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Weiner G;
XX
DR WPI; 1999-620169/53.
XX
PT Novel synergistic combinations of immunostimulatory oligonucleotides
PT and immunopotentiating cytokines are useful for stimulating the immune
PT system -
XX
PS Example 8; Page 80; 91pp; English.
XX
CC Sequences Z41856-Z41949 are phosphorothioate CpG oligonucleotides which
CC are used in the invention to induce interleukin-12 (IL-12) secretion
CC from human PBMC. The invention comprises stimulating an immune response
CC in a subject comprising administering to a subject exposed to an antigen,
CC an immunopotentiating cytokine and an immunostimulatory CpG
CC oligonucleotide to induce a synergistic antigen specific immune response.
CC The methods are useful for treating cancer by stimulating an antigen
CC specific immune response against a cancer antigen. The methods can also
CC be used to treat neoplastic disorders in humans, including but not
CC limited to: sarcoma, carcinoma, fibroma, Lymphoma, melanoma,
CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC for treating infectious diseases, e.g. viral diseases such as HIV,
CC bacterial diseases, and fungal diseases. The methods may also be used to
CC treat allergic diseases, e.g. asthma. The methods and compositions may
CC also be applied to treat cancer and tumours in non human subjects,
CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC be treated and include leukaemia, haemangiopericytoma and bovine ocular
CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC caused by the bacterium Corynebacterium pseudotuberculosis, and
CC contagious lung tumour of sheep caused by jaagsiekte may also be treated.
CC CpG oligonucleotides can be useful in activating B cells, NK cells, and
CC antigen presenting cells, such as monocytes and macrophages. CpG
CC oligonucleotides enhance antibody dependent cellular cytotoxicity and can
CC be used as an adjuvant in conjunction with tumour antigens to protect
CC against a tumour challenge.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcccagcgtgcgccat 18
||||||||||||||||||
Db 1 tctcccagcgtgcgccat 18

RESULT 8
Z41948
ID Z41948 standard; DNA; 18 BP.
XX
AC Z41948;
XX
DT 24-JAN-2000 (first entry)
XX
DE IL-12 secretion inducing CpG oligonucleotide 93.
XX
KW CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW antigen presenting cell; infection; allergic disease.
XX
OS Synthetic.
XX
PN WO9951259-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07335.
XX
PR 03-APR-1998; 98US-0080729.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Weiner G;
XX
DR WPI; 1999-620169/53.

```
XX
PT   Novel synergistic combinations of immunostimulatory oligonucleotides
PT   and immunopotentiating cytokines are useful for stimulating the immune
PT   system -
XX
PS   Example 8; Page 88; 91pp; English.
XX
CC   Sequences Z41856-Z41949 are phosphorothioate CpG oligonucleotides which
CC   are used in the invention to induce interleukin-12 (IL-12) secretion
CC   from human PBMC. The invention comprises stimulating an immune response
CC   in a subject comprising administering to a subject exposed to an antigen,
CC   an immunopotentiating cytokine and an immunostimulatory CpG
CC   oligonucleotide to induce a synergistic antigen specific immune response.
CC   The methods are useful for treating cancer by stimulating an antigen
CC   specific immune response against a cancer antigen. The methods can also
CC   be used to treat neoplastic disorders in humans, including but not
CC   limited to: sarcoma, carcinoma, fibroma, Lymphoma, melanoma,
CC   neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC   for treating infectious diseases, e.g. viral diseases such as HIV,
CC   bacterial diseases, and fungal diseases. The methods may also be used to
CC   treat allergic diseases, e.g. asthma. The methods and compositions may
CC   also be applied to treat cancer and tumours in non human subjects,
CC   e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC   be treated and include leukaemia, haemangiopericytoma and bovine ocular
CC   neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC   caused by the bacterium Corynebacterium pseudotuberculosis, and
CC   contagious lung tumour of sheep caused by jaagsiekte may also be treated.
CC   CpG oligonucleotides can be useful in activating B cells, NK cells, and
CC   antigen presenting cells, such as monocytes and macrophages. CpG
CC   oligonucleotides enhance antibody dependent cellular cytotoxicity and can
CC   be used as an adjuvant in conjunction with tumour antigens to protect
CC   against a tumour challenge.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT   9
X78803
ID   X78803 standard; DNA; 18 BP.
XX
AC   X78803;
XX
DT   06-SEP-1999  (first entry)
XX
DE   HPV fusion protein CpG oligonucleotide 2.
XX
KW   Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW   immunological fusion partner; CpG oligonucleotide; immune response;
KW   HPV antigen; prevention; treatment; primer; ss.
XX
OS   Synthetic.
OS   Human papillomavirus.
XX
PN   WO9933868-A2.
XX
PD   08-JUL-1999.
XX
PF   18-DEC-1998;   98WO-EP08563.
XX
PR   24-DEC-1997;   97GB-0027262.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Dalemans WLJ,  Gerard CMG;
XX
DR   WPI; 1999-405485/34.
XX
PT   Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT   induce immune response to HPV
XX
PS   Claim 11; Page 37; 62pp; English.
XX
CC   X78791-X78801 represent nucleic acid sequences which encode novel
CC   constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC   HPV (represented in Y25375-Y25386). These constructs are optionally
CC   linked to an immunological fusion partner and an immunomodulatory CpG
CC   oligonucleotide. The products of the invention can be used to induce an
CC   immune response in a patient to an HPV antigen. They can also be used
CC   for preventing or treating HPV induced tumours. This sequence represents
CC   a CpG oligonucleotide which is used in the method of the invention.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT  10
X88537
ID   X88537 standard; DNA; 18 BP.
XX
AC   X88537;
XX
DT   10-SEP-1999  (first entry)
XX
DE   Cytosine-guanosine dinucleotide motif oligonucleotide #4.
XX
KW   Cytosine-guanosine dinucleotide motif; CpG; immunomodulation;
KW   unmethylated; vaccine; immunostimulation; immune response;
KW   T-independent type 1 antigen; T-independent type 2 antigen;
KW   polysaccharide conjugate antigen; ss.
XX
OS   Synthetic.
XX
PN   WO9933488-A2.
XX
PD   08-JUL-1999.
XX
PF   18-DEC-1998;   98WO-EP08562.
XX
PR   24-DEC-1997;   97GB-0027262.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Dalemans WLJ,  Laferriere CAJ,  Prieels J;
XX
DR   WPI; 1999-405369/34.
XX
PT   A vaccine composition for inducing a immune response to
PT   T-independent type 1 or type 2 antigen or polysaccharide conjugate
PT   antigen
XX
PS   Claim 6; Page 31; 35pp; English.
XX
CC   The present invention describes a formulation (A) comprising a
CC   cytosine-guanosine dinucleotide motif (CpG) oligonucleotide and
CC   T-independent type 1 or type 2 antigens or polysaccharide conjugate
CC   antigen. The present sequence represent a specifically claimed CpG
CC   oligonucleotide. A vaccine composition comprising the formulation is
CC   used for inducing a immune response to T-independent type 1 or type 2
CC   antigen or polysaccharide conjugate antigen. The use of
```

```
CC   immunostimulatory CpG oligonucleotide acts as an adjuvant to
CC   pneumococcal polysaccharides.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT  11
X33514
ID   X33514 standard; DNA; 18 BP.
XX
AC   X33514;
XX
DT   07-JUL-1999  (first entry)
XX
DE   BCL2-targeted antisense oligonucleotide SEQ ID NO:45.
XX
KW   Conbinatorial antisense library; oligonucleotide analogue; RNase;
KW   ribozyme; cleavage; anchor; binding; target RNA; ss.
XX
OS   Synthetic.
XX
PN   WO9918238-A1.
XX
PD   15-APR-1999.
XX
PF   28-SEP-1998;   98WO-US20361.
XX
PR   18-AUG-1998;   98US-0136080.
PR   02-OCT-1997;   97US-0060673.
XX
PA   (OASI-) OASIS BIOSCIENCES INC.
XX
PI   Arnold LJ,  Brown BD,  Riley TA;
XX
DR   WPI; 1999-264039/22.
XX
PT   Oligonucleotide analog compositions capable of coupling to form
PT   antisense molecules
XX
PS   Example 9; Page 45; 71pp; English.
XX
CC   The present invention describes a composition comprising two
CC   oligonucleotide analogues, each having a binding domain and a coupling
CC   moiety, where the binding domains are capable of hybridizing to a target
CC   polynucleotide and the coupling moieties are capable of coupling to each
CC   other in the absence of a target molecule. The composition/compound is
CC   used to cleave an RNA target. The compositions can be used to determine
CC   an optimal antisense site for a given mRNA or an optimal ribozyme
CC   cleavage site for a target RNA. By separating the antisense molecules
CC   into two or more pieces, a comprehensive antisense library can be
CC   prepared in advance, rather than synthesizing a plurality of candidate
CC   antisense molecules as needed. A complete library of every possible
CC   17-mer oligonucleotide, using the four natural bases, would consist of
CC   417 (or about 1.7 x 1010) molecules. By providing the antisense molecules
CC   in at least two components, e.g. a library of 8-mers and a library of
CC   9-mers, assembled quickly as needed, the library size is reduced to 48 +
CC   49, or 327 650 molecules. The complexity of the library can be further
CC   reduced by substituting one or more universal or degenerate bases for
CC   some of the natural bases. The present sequence represents an
CC   oligonucleotide, which is used in an example from the present invention.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT  12
X23693
ID   X23693 standard; DNA; 18 BP.
XX
AC   X23693;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 146.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US18084.
XX
PR   02-SEP-1997;   97US-0923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides  - useful for characterizing a sample of target
PT   deletion oligonucleotides
XX
PS   Example 9; Page 152; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in X23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence
CC   for its reverse complement is not modified, the method may be performed
CC   using oligodeoxynucleotides.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT  13
X27536/c
ID   X27536 standard; RNA; 18 BP.
XX
AC   X27536;
XX
DT   27-MAY-1999  (first entry)
XX
DE   Synthetic RNA sequence produced by the method of the invention.
XX
KW   Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
KW   cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
XX
OS   Synthetic.
XX
PN   WO9909044-A1.
XX
PD   25-FEB-1999.
XX
PF   17-AUG-1998;   98WO-EP05215.
XX
PR   18-AUG-1997;   97CH-0001931.
XX
PA   (JENN/) JENNY L.
PA   (PITS/) PITSCH S.
PA   (WEIS/) WEISS P A.
XX
PI   Jenny L,  Pitsch S,  Weiss PA;
XX
DR   WPI; 1999-180963/15.
XX
PT   2-Silyloxymethyl ribonucleosides and their phosphonate derivatives
PT   - have high purity, use in machine synthesis of ribonucleic acids,
PT   enable longer oligonucleotide chain construction, and larger amounts
XX
PS   Example 7; Page 26; 38pp; English.
XX
CC   The invention relates to silyloxymethyl protected D- or L-ribonucleosides
CC   and their phosphonates (I), and silyloxymethyl halides (II). (I) are
CC   intermediates for synthesis of RNA-oligonucleotides with predetermined
CC   nucleotide sequence, particularly by machine synthesis. The groups
CC   specified above, apart from those on silyl, are those particularly for
CC   the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
CC   products in diagnosis, therapy, and as research tools, are well known,
CC   and are not dealt with in detail. (II) is an intermediate for (I). The
CC   silyloxymethyl halide reagent is easy to prepare, and yields are high.
CC   Introduction of the silyloxymethyl group into the ribonucleoside is
CC   simple and rapid, and the acetal bond formed does not migrate,
CC   eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC   The methylenedioxy group spacer between the silyl group and nucleoside
CC   ring results in less steric hindrance than bulky direct silyloxy
CC   linkages, enabling first, a range of choices for the silyl substituents,
CC   to provide, e.g., acid or base stability; and second, higher yields in
CC   coupling. Purer products are therefore obtained than in prior art,
CC   enabling larger quantities and longer chains of oligoribonucleotides to
CC   be synthesised successfully, and in shorter times.
XX
SQ   Sequence 18 BP; 4 A; 4 C; 8 G; 2 U; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     18 TCTCCCAGCGTGCGCCAT 1


RESULT  14
X18702
ID   X18702 standard; DNA; 18 BP.
XX
AC   X18702;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Target bcl-2 antisense oligonucleotide BCL-2.
XX
KW   Cellular adhesion protein; proliferation; antisense oligonucleotide;
KW   alimentary canal; transport; gastrointestinal mucosa; cancer;
KW   Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW   HIV; inflammation; ss.
XX
OS   Synthetic.
XX
PN   WO9901579-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US13574.
XX
PR   01-JUL-1997;   97US-0886829.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Hardee G,  Teng C;
XX
DR   WPI; 1999-106077/09.
XX
PT   Composition comprising nucleic acid and penetration enhancer - used
PT   particularly for delivering therapeutic antisense oligonucleotides
PT   across the gastrointestinal mucosa, provides high bioavailability
XX
PS   Example 2; Page 86; 115pp; English.
XX
CC   A pharmaceutical composition has been developed which comprises a
CC   nucleic acid and at least one penetration enhancer. The compositions are
CC   used: (i) to treat or prevent any disease or disorder that can be
CC   treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC   beta-thalassemia, malaria, viral infections (including human immune
CC   deficiency virus (HIV)), inflammation, in human or animal medicine;
CC   (ii) to investigate the role of a gene or gene product in non-human
CC   animals; and (iii) to modulate gene expression in cells, tissues or
CC   organs. The compositions provide bioavailability of at least 15,
CC   preferably 17-35,%. The penetration enhancer improves: (i) transport of
CC   the nucleic acid across the mucosa of the alimentary canal and into
CC   cells; and (ii) increases stability of the nucleic acid. Oral
CC   administration avoids the complications and expense of intravenous or
CC   other methods of administration. X18669 to X18799 and X18801 represent
CC   antisense oligonucleotides which can be used as the nucleic acid in
CC   the method of the invention.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT  15
V99434
ID   V99434 standard; DNA; 18 BP.
XX
AC   V99434;
```

```
XX
DT   22-MAR-1999  (first entry)
XX
DE   Antisense oligonucleotide directed against human bcl-2 gene.
XX
KW   Antisense oligonucleotide; human bcl-2 gene; phosphorothioate;
KW   phosphodiester; lipid-encapsulation; tumour; aberrant gene expression;
KW   treatment; inflammation; infection; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..18
FT                   /*tag=  a
FT                   /note= "phosphorothioate or phosphodiester bonds"
XX
PN   WO9851278-A2.
XX
PD   19-NOV-1998.
XX
PF   14-MAY-1998;   98WO-CA00485.
XX
PR   14-MAY-1997;   97US-0856374.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Ansell SM,  Cullis P,  Debeyer D,  Harasym T,  Hope MJ;
PI   Klimuk SK,  Scherrer P,  Semple SC;
XX
DR   WPI; 1999-045179/04.
XX
PT   Composition containing lipid-encapsulated therapeutic agent -
PT   useful, e.g. for delivering antisense molecules or ribozymes or
PT   treating diseases associated with aberrant gene expression
XX
PS   Disclosure; Page 23; 98pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide directed
CC   against the human bcl-2 gene. The oligonucleotide can have either
CC   phosphorothioate or phosphodiester bonds. The oligonucleotide is
CC   lipid-encapsulated using the method of the invention. A composition
CC   comprising lipid-encapsulated particles of a therapeutic agent,
CC   e.g. antisense oligonucleotides, is prepared by mixing at least
CC   2 lipids with buffered aqueous solution of charged therapeutic
CC   agent to form an intermediate mixture of lipid-encapsulated particles,
CC   and changing the pH of the mixture to neutralise at least some of the
CC   external surface charges on the particles. One lipid has a
CC   (de)protonatable group with Ka such that the lipid is charged at a
CC   first pH but neutral at a second pH (particularly near physiological pH)
CC   and the buffer maintains this lipid in the charged form (i.e. cationic
CC   when the therapeutic agent is anionic in the buffer, or vice versa). The
CC   second lipid prevents particle aggregation during formation of the
CC   lipid-therapeutic agent particles. The composition is used to introduce
CC   therapeutic agents into cells, in vivo or in vitro, particularly to
CC   treat or prevent diseases associated with aberrant gene expression in
CC   mammals, specifically tumours, inflammation or infection.
XX
SQ   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 18;  DB 20;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18



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Job time: 16673 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 16:28:02 ; Search time 75.06 Seconds
(without alignments)
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Title: US-09-369-941-1
Perfect score: 18
Sequence: 1 tctcccagcgtgcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	2	US-08-217-082A-17	Sequence 17, Appl
	2	18	100.0	18	3	US-08-465-485A-17	Sequence 17, Appl
	3	18	100.0	18	3	US-08-465-485A-24	Sequence 24, Appl
	4	18	100.0	18	5	US-09-080-285-17	Sequence 17, Appl
	5	18	100.0	18	5	US-09-080-285-24	Sequence 24, Appl
	6	18	100.0	18	5	US-09-249-730-218	Sequence 218, App
c	7	18	100.0	27	1	US-08-410-804-13	Sequence 13, Appl
c	8	18	100.0	27	2	US-08-607-269-8	Sequence 8, Appli
c	9	18	100.0	27	2	US-08-259-514-13	Sequence 13, Appl
c	10	18	100.0	27	3	US-08-858-311-13	Sequence 13, Appl
c	11	18	100.0	27	6	PCT-US95-04600-8	Sequence 8, Appli
c	12	18	100.0	35	2	US-08-217-082A-2	Sequence 2, Appli
c	13	18	100.0	35	3	US-08-465-485A-2	Sequence 2, Appli
c	14	18	100.0	35	5	US-09-080-285-2	Sequence 2, Appli
c	15	18	100.0	615	3	US-08-465-485A-22	Sequence 22, Appl
c	16	18	100.0	615	5	US-09-080-285-22	Sequence 22, Appl
c	17	18	100.0	623	7	5506344-3	Patent No. 5506344
c	18	18	100.0	717	3	US-08-465-485A-20	Sequence 20, Appl
c	19	18	100.0	717	5	US-09-080-285-20	Sequence 20, Appl
c	20	18	100.0	760	2	US-08-405-702A-11	Sequence 11, Appl
c	21	18	100.0	831	7	5459251-3	Patent No. 5459251
c	22	18	100.0	831	7	5506344-4	Patent No. 5506344
c	23	18	100.0	911	6	PCT-US93-06251-3	Sequence 3, Appli
c	24	18	100.0	1846	3	US-08-365-486A-16	Sequence 16, Appl
c	25	18	100.0	4825	7	5459251-1	Patent No. 5459251
c	26	18	100.0	5086	3	US-08-465-485A-19	Sequence 19, Appl
c	27	18	100.0	5086	3	US-08-365-486A-14	Sequence 14, Appl
c	28	18	100.0	5086	5	US-09-080-285-19	Sequence 19, Appl
c	29	18	100.0	5086	6	PCT-US93-05651-4	Sequence 4, Appli
c	30	18	100.0	5086	6	PCT-US93-06251-2	Sequence 2, Appli
c	31	18	100.0	5104	7	5506344-1	Patent No. 5506344
	32	17	94.4	17	2	US-08-217-082A-9	Sequence 9, Appli
c	33	15.4	85.6	33	5	US-08-650-726-1	Sequence 1, Appli
	34	15	83.3	17	2	US-08-217-082A-8	Sequence 8, Appli
	35	15	83.3	17	4	US-08-877-831-1	Sequence 1, Appli
c	36	14.8	82.2	335	7	5175102-1	Patent No. 5175102
	37	14.4	80.0	6002	2	US-08-698-551-15	Sequence 15, Appl
	38	14.4	80.0	6002	3	US-08-602-228-15	Sequence 15, Appl
	39	14.4	80.0	6002	3	US-08-839-032A-15	Sequence 15, Appl
c	40	14.4	80.0	34303	4	US-08-735-609-4	Sequence 4, Appli
c	41	14.4	80.0	34303	4	US-08-735-609-4	Sequence 4, Appli
c	42	14.4	80.0	34303	5	US-09-315-372-4	Sequence 4, Appli
c	43	14.4	80.0	34303	5	US-09-244-752-4	Sequence 4, Appli
c	44	14.4	80.0	34303	5	US-09-245-497-4	Sequence 4, Appli
c	45	14.4	80.0	34382	3	US-08-374-483-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT   1
US-08-217-082A-17
; Sequence 17, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  Synthetic DNA
US-08-217-082A-17
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  Query Match             100.0%;  Score 18;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   2
US-08-465-485A-17
; Sequence 17, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-465-485A-17


  Query Match             100.0%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   3
US-08-465-485A-24
; Sequence 24, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
;    FEATURE:
;      NAME/KEY:  Modified_base
;      LOCATION:  16..17
;      OTHER INFORMATION:  Last two internucleoside linkages are
;      OTHER INFORMATION:  phosphorothioates
US-08-465-485A-24


  Query Match             100.0%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   4
US-09-080-285-17
; Sequence 17, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
```

```
;       ADDRESSEE:  P.C.
;       STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;       CITY:  Arlington
;       STATE:  Virginia
;       COUNTRY:  U.S.A.
;       ZIP:  22202
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/080,285
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/465,485
;       FILING DATE:  05-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/124,256
;       FILING DATE:  20-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/840,716
;       FILING DATE:  21-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/288,692
;       FILING DATE:  22-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fortney, Andrew D.
;       REGISTRATION NUMBER:  34,600
;       REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (408) 436-2070
;       TELEFAX:  (408) 436-2075
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-080-285-17


  Query Match             100.0%;  Score 18;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   5
US-09-080-285-24
; Sequence 24, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA
;    ANTI-SENSE:  YES
;    FEATURE:
;      NAME/KEY:  Modified_base
;      LOCATION:  16..17
;      OTHER INFORMATION:  Last two internucleoside linkages are
;      OTHER INFORMATION:  phosphorothioates
US-09-080-285-24


  Query Match             100.0%;  Score 18;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 TCTCCCAGCGTGCGCCAT 18


RESULT   6
US-09-249-730-218
; Sequence 218, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping H.
;  TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
;  TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
;  FILE REFERENCE: 032396-040
;  CURRENT APPLICATION NUMBER: US/09/249,730
;  CURRENT FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 220
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human
US-09-249-730-218


  Query Match             100.0%;  Score 18;  DB 5;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db      1 tctcccagcgtgcgccat 18


RESULT   7
US-08-410-804-13/c
; Sequence 13, Application US/08410804
; Patent No. 5632994
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  FAS ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cathryn Campbell
;      STREET:  4370 La Jolla Village Drive. Ste 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,804
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/259,514
;      FILING DATE:  14-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1389
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-410-804-13


  Query Match            100.0%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT   8
US-08-607-269-8/c
; Sequence 8, Application US/08607269
; Patent No. 5702897
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  Interaction of Proteins Involved in a
;    TITLE OF INVENTION:  Cell Death Pathway
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/607,269
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/226,876
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 9882
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-607-269-8


  Query Match            100.0%;  Score 18;  DB 2;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT   9
US-08-259-514-13/c
; Sequence 13, Application US/08259514
; Patent No. 5747245
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  FAS ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cathryn Campbell
;      STREET:  4370 La Jolla Village Drive. Ste 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/259,514
;      FILING DATE:  14-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 9954
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
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;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-259-514-13


  Query Match             100.0%;  Score 18;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT  10
US-08-858-311-13/c
; Sequence 13, Application US/08858311
; Patent No. 5876939
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John C.
;    APPLICANT:  Sato, Takaaki
;    TITLE OF INVENTION:  FAS ASSOCIATED PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cathryn Campbell
;      STREET:  4370 La Jolla Village Drive. Ste 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/858,311
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/410,804
;      FILING DATE:  27-MAR-1995
;      APPLICATION NUMBER:  US 08/259,514
;      FILING DATE:  14-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1389
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-858-311-13


  Query Match             100.0%;  Score 18;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT  11
PCT-US95-04600-8/c
; Sequence 8, Application PC/TUS9504600
;  GENERAL INFORMATION:
;    APPLICANT:  LA JOLLA CANCER RESEARCH FOUNDATION
;    TITLE OF INVENTION:  Interaction of Proteins Involved in
;    TITLE OF INVENTION:  a Cell Death Pathway
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04600
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Imbra, Richard J.
;      REGISTRATION NUMBER:  37,643
;      REFERENCE/DOCKET NUMBER:  FP-LJ 1361
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-04600-8


  Query Match             100.0%;  Score 18;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     25 TCTCCCAGCGTGCGCCAT 8


RESULT  12
US-08-217-082A-2/c
; Sequence 2, Application US/08217082A
; Patent No. 5734033
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
;    TITLE OF INVENTION:  GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  224 Airport Parkway
;      CITY:  San Jose
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  95110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,082A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-067-55 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-08-217-082A-2


  Query Match             100.0%;  Score 18;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     35 TCTCCCAGCGTGCGCCAT 18


RESULT  13
US-08-465-485A-2/c
; Sequence 2, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-08-465-485A-2


  Query Match             100.0%;  Score 18;  DB 3;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     35 TCTCCCAGCGTGCGCCAT 18


RESULT  14
US-09-080-285-2/c
; Sequence 2, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-09-080-285-2


  Query Match             100.0%;  Score 18;  DB 5;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     35 TCTCCCAGCGTGCGCCAT 18


RESULT  15
US-08-465-485A-22/c
; Sequence 22, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  615 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..615
US-08-465-485A-22


  Query Match             100.0%;  Score 18;  DB 3;  Length 615;
  Best Local Similarity   100.0%;  Pred. No. 0.9;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tctcccagcgtgcgccat 18
          ||||||||||||||||||
Db     18 TCTCCCAGCGTGCGCCAT 1


Search completed:  December  4, 2000, 21:08:04
Job time:  16802 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 21:06:39 ; Search time 1141.84 Seconds
(without alignments)
108.295 Million cell updates/sec

Title: US-09-369-941-2
Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
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113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16.8	84.0	464	2	AA171941	AA171941 zp24f01.s
c 2	16.8	84.0	546	19	AW065908	AW065908 687002G08
c 3	16.8	84.0	797	113	CNS02NO6	AL205647 Tetraodon
4	16.8	84.0	821	114	CNS03G84	AL242653 Tetraodon
5	16.8	84.0	992	114	CNS040Q4	AL269221 Tetraodon
6	16.8	84.0	994	114	CNS042IL	AL271542 Tetraodon
7	16.4	82.0	824	113	CNS01XPZ	AL172016 Tetraodon
c 8	16.4	82.0	1015	115	CNS05NA3	AL345108 Tetraodon
9	16	80.0	179	19	AV525865	AV525865 AV525865
10	15.8	79.0	254	30	BB342084	BB342084 BB342084
11	15.8	79.0	262	30	BB398655	BB398655 BB398655
c 12	15.8	79.0	392	8	AI077366	AI077366 oy87e11.x
c 13	15.8	79.0	408	8	AI086210	AI086210 ow90d05.s
c 14	15.8	79.0	490	19	AW063142	AW063142 TN0287 KR
15	15.8	79.0	509	98	AQ478992	AQ478992 RPCI-11-2
c 16	15.8	79.0	717	114	CNS04SXG	AL305773 Tetraodon
17	15.8	79.0	934	99	AQ573722	AQ573722 nbxb0084B
18	15.8	79.0	938	114	CNS03I44	AL245101 Tetraodon
c 19	15.8	79.0	992	114	CNS04Q70	AL302229 Tetraodon
c 20	15.4	77.0	219	115	FR0021650	AL014523 F.rubripe
21	15.4	77.0	279	100	AQ651891	AQ651891 Sheared D
c 22	15.4	77.0	302	115	FR0023000	AL015860 F.rubripe
c 23	15.4	77.0	311	28	BB234999	BB234999 BB234999
c 24	15.4	77.0	317	115	FR0021653	AL014526 F.rubripe
25	15.4	77.0	347	115	FR0023012	AL015871 F.rubripe
26	15.4	77.0	395	115	FR0021632	AL014505 F.rubripe
27	15.4	77.0	467	9	AI181400	AI181400 uc59c05.r
28	15.4	77.0	537	13	AI812316	AI812316 10G3 Pine
c 29	15.4	77.0	552	115	FR0021654	AL014527 F.rubripe
30	15.4	77.0	554	115	FR0021629	AL014502 F.rubripe
31	15.4	77.0	580	115	FR0023009	AL015869 F.rubripe
c 32	15.4	77.0	584	115	FR0021635	AL014508 F.rubripe
33	15.4	77.0	597	115	FR0021641	AL014514 F.rubripe
c 34	15.4	77.0	598	115	FR0021637	AL014510 F.rubripe
35	15.4	77.0	609	115	FR0022992	AL015852 F.rubripe
36	15.4	77.0	612	115	FR0021647	AL014520 F.rubripe
c 37	15.4	77.0	629	34	BE195266	BE195266 HVSMEh008
c 38	15.4	77.0	658	9	AI234463	AI234463 EST366 Ma
c 39	15.2	76.0	151	4	AA494709	AA494709 fa10h06.r
c 40	15.2	76.0	189	12	AI771817	AI771817 EST252917
41	15.2	76.0	253	30	BB385734	BB385734 BB385734
42	15.2	76.0	272	7	AA958394	AA958394 ua11c12.r
43	15.2	76.0	273	89	AQ105312	AQ105312 HS_3020_B
44	15.2	76.0	277	27	BB110967	BB110967 BB110967
45	15.2	76.0	278	28	BB230155	BB230155 BB230155

ALIGNMENTS

RESULT 1
AA171941

LOCUS AA171941 464 bp mRNA EST 23-DEC-1996
DEFINITION zp24f01.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610393 3' similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION AA171941
VERSION AA171941.1 GI:1751000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 464)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 360.
FEATURES Location/Qualifiers
source 1. .464
/organism="Homo sapiens"
/db_xref="GDB:4625652"
/db_xref="taxon:9606"
/clone="IMAGE:610393"
/clone_lib="Stratagene neuroepithelium (#937231)"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2 cells (Ntera-2/c1.D1) induced with Retinoic Acid for 24 hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT 109 a 105 c 100 g 148 t 2 others
ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 464;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 tccatgacgttcctgacgtt 20
          ||||||| |||||||| |||
Db    431 TCCATGAGGTTCCTGAAGTT 450
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RESULT 2
AW065908/c
LOCUS AW065908 546 bp mRNA EST 30-MAR-2000
DEFINITION 687002G08.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.
ACCESSION AW065908
VERSION AW065908.1 GI:6020980
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
REFERENCE 1 (bases 1 to 546)
AUTHORS Walbot,V.

```
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 687002  row: G  column: 08.
FEATURES             Location/Qualifiers
     source          1. .546
                     /organism="Zea mays"
                     /cultivar="Illinois High Oil"
                     /db_xref="taxon:4577"
                     /clone_lib="687 - Early embryo from Delaware"
                     /tissue_type="embryo"
                     /dev_stage="14, 21, 28, and 35 days after pollination"
                     /lab_host="E. coli SOLR"
                     /note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
                     ; Site_2: EcoRI; Library was prepared by Statagene using
                     the Uni-ZAP XR system (Stratagene BN937328-12). Clones
                     were picked by a Q-bot after blue/white selection
                     (ampicillin resistance - use 100 micrograms/microliter).
                     Developed from a pool of equal amounts of RNA from
                     developing embryos sampled at 14, 21, 28 and 35 days after
                     pollination of the Illinois High Oil Maize Strain Cycle
                     90. This closed strain has been selected for high oil
                     concentration for 90 generations and originates from the
                     1890s era open pollinated variety Burr's White"
BASE COUNT      113 a    183 c    156 g     94 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 19;  Length 546;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||||||  ||
Db     229 TCCATGACGTTCCTGATCTT 210


RESULT   3
CNS02NO6/c
LOCUS       CNS02NO6      797 bp    DNA             GSS       14-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            151L08 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL205647
VERSION     AL205647.1  GI:7864466
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 797)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 797)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .797
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="151L08"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG151DF04LP1-end : T7"
BASE COUNT      192 a    204 c    209 g    177 t     15 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 113;  Length 797;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||| ||||||||||| ||||
Db     604 TCCAAGACGTTCCTGGCGTT 585


RESULT   4
CNS03G84
LOCUS       CNS03G84      821 bp    DNA             GSS       17-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            023N02 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL242653
VERSION     AL242653.1  GI:7963422
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 821)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 821)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="023N02"
                     /clone_lib="G"
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                     /note="Genoscope sequence ID : C0BG023DG01LP1~end : T7"
BASE COUNT      217 a    145 c    172 g    279 t      8 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 114;  Length 821;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||| ||||||| ||||||||
Db    627 TCCTTGACGTTACTGACGTT 646


RESULT   5
CNS040Q4
LOCUS       CNS040Q4      992 bp    DNA             GSS       18-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            073A13 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL269221
VERSION     AL269221.1  GI:7991098
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 992)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 992)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 992)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .992
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="073A13"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG073AA07LP1~end : T7"
BASE COUNT      242 a    184 c    211 g    337 t     18 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 114;  Length 992;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||| ||||||| ||||||||
Db    815 TCCTTGACGTTACTGACGTT 834


RESULT   6
CNS042IL
LOCUS       CNS042IL      994 bp    DNA             GSS       18-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            077D02 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL271542
VERSION     AL271542.1  GI:7993521
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 994)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 994)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .994
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="077D02"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG077DB01LP1~end : T7"
BASE COUNT      309 a    199 c    226 g    256 t      4 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 114;  Length 994;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||| | ||||
Db    206 TCCATGACGTTCCAGCCGTT 225


RESULT   7
CNS01XPZ
LOCUS       CNS01XPZ      824 bp    DNA             GSS       12-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            202P06 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL172016
VERSION     AL172016.1  GI:7810073
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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REFERENCE   1  (bases 1 to 824)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 824)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 824)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .824
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="202P06"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG202DH03SP1~end :
                     PUC-Ori"
BASE COUNT      167 a    236 c    287 g    104 t     30 others
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 113;  Length 824;
  Best Local Similarity   94.4%;  Pred. No. 3.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacg 18
          ||||| ||||||||||||
Db    232 TCCATCACGTTCCTGACG 249


RESULT   8
CNS05NA3/c
LOCUS       CNS05NA3     1015 bp    DNA             GSS       26-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence SP6 end of clone
            035P01 of library B from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL345108
VERSION     AL345108.1  GI:8238878
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1015)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="035P01"
                     /clone_lib="B"
                     /note="Genoscope sequence ID : C0BB035CH01B1~end : SP6"
BASE COUNT      253 a    268 c    261 g    214 t     19 others
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 115;  Length 1015;
  Best Local Similarity   94.4%;  Pred. No. 4e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 catgacgttcctgacgtt 20
          |||||||||||||| |||
Db    234 CATGACGTTCCTGATGTT 217


RESULT   9
AV525865
LOCUS       AV525865      179 bp    mRNA            EST       21-JUL-2000
DEFINITION  AV525865 Arabidopsis thaliana aboveground organs two to six-week
            old Arabidopsis thaliana cDNA clone APD31f02R 5', mRNA sequence.
ACCESSION   AV525865
VERSION     AV525865.1  GI:8685393
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 179)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
  JOURNAL   DNA Res. 7, 175-180 (2000)
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .179
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="APD31f02R"
                     /clone_lib="Arabidopsis thaliana aboveground organs two to
                     six-week old"
                     /tissue_type="aboveground organs"
                     /dev_stage="two to six-week old"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       47 a     35 c     48 g     49 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 19;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 tgacgttcctgacgtt 20
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          ||||||||||||||||
Db    144 TGACGTTCCTGACGTT 159


RESULT 10
BB342084
LOCUS       BB342084      254 bp    mRNA            EST       12-JUL-2000
DEFINITION  BB342084 RIKEN full-length enriched, 10 days neonate cerebellum Mus
            musculus cDNA clone B930035G08 3', mRNA sequence.
ACCESSION   BB342084
VERSION     BB342084.1  GI:9051790
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 254)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .254
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="B930035G08"
                     /clone_lib="RIKEN full-length enriched, 10 days neonate
                     cerebellum"
                     /sex="mixed"
                     /tissue_type="cerebellum"
                     /dev_stage="10 days neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGACAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
BASE COUNT       65 a     50 c     45 g     94 t
ORIGIN


  Query Match             79.0%;  Score 15.8;  DB 30;  Length 254;
  Best Local Similarity   89.5%;  Pred. No. 6.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 ccatgacgttcctgacgtt 20
           |||||  ||||||||||||
Db     108 CCATGGAGTTCCTGACGTT 126


RESULT 11
BB398655
LOCUS       BB398655      262 bp    mRNA            EST       15-JUL-2000
DEFINITION  BB398655 RIKEN full-length enriched, ES cells Mus musculus cDNA
            clone C330009E15 3', mRNA sequence.
ACCESSION   BB398655
VERSION     BB398655.1  GI:9218051
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 262)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
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           Carninci,P. and Hayashizaki,Y.
           High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           19-44 (1999)
           Please visit our web site (http://genome.rtc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .262
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="C330009E15"
                     /clone_lib="RIKEN full-length enriched, ES cells"
                     /cell_type="ES cells"
                     /lab_host="SOLR"
                     /note="Site_1: XhoI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 5.0 and subtraction to Rot = 25.0. Second strand
                     cDNA was prepared with the primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']."
BASE COUNT       53 a     63 c     42 g    103 t      1 others
ORIGIN


  Query Match             79.0%;  Score 15.8;  DB 30;  Length 262;
  Best Local Similarity   89.5%;  Pred. No. 6.9e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgt 19
           ||||||||  |||||||||
Db      49 TCCATGACACTCCTGACGT 67


RESULT  12
AI077366/c
LOCUS       AI077366      392 bp    mRNA            EST       29-SEP-1998
DEFINITION  oy87e11.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1672844 3', mRNA sequence.
ACCESSION   AI077366
VERSION     AI077366.1  GI:3411774
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 904   Std Error: 0.00
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            High quality sequence stop: 294.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:1672844"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      100 a     86 c     88 g    118 t
ORIGIN


  Query Match             79.0%;  Score 15.8;  DB 8;  Length 392;
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  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 ccatgacgttcctgacgtt 20
           |||||||||||||||  | |
Db     202 CCATGACGTTCCTGAAGCT 184


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LOCUS       AI086210      408 bp    mRNA            EST       28-AUG-1998
DEFINITION  ow90d05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1654089 3', mRNA sequence.
ACCESSION   AI086210
VERSION     AI086210.1  GI:3424633
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 720   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 346.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      105 a     91 c     94 g    118 t
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DEFINITION  TN0287 KRIBB Human TN intrathymic T-cell cDNA library Homo sapiens
            cDNA 3', mRNA sequence.
ACCESSION   AW063142
VERSION     AW063142.1  GI:8887191
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Goh,S.-H., Park,J.-H., Lee,I.-C., Park,J.-H., Hur,C.-G., Yoo,H.-S.,
            Lee,C.-C. and Kim,Y.-S.
  TITLE     Expressed sequence tags from three developmental stages of human
            intrathymic T-cells
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Sung-Ho Goh
            Genome Center
            Korea Research Institute of Bioscience and Biotechnology
            Oun-dong 52, Yu Sung-Gu, Daejon 305-333, Republic of Korea
            Tel: 82-42-860-4473
            Fax: 82-42-860-4479
            Email: gohsh@mail.kribb.re.kr
            Seq primer: T7
            High quality sequence stop: 490
            POLYA=No.
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                     /db_xref="taxon:9606"
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                     /cell_type="Intrathymic T-cell"
                     /dev_stage="CD3-4-8- triple negative stage"
                     /note="Vector: pGEM-T; cDNA was made from total
                     cytoplasmic RNA of sorted human intrathymic CD3-4-8-
                     T-cell, adaptor ligated, amplified with PCR, and cloned
                     into pGEM-T vector."
BASE COUNT      103 a    142 c    161 g     83 t      1 others
ORIGIN


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DEFINITION  RPCI-11-254K21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-254K21
            , DNA sequence.
ACCESSION   AQ478992
VERSION     AQ478992.1  GI:4661111
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
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BASE COUNT      134 a    127 c    145 g    103 t
ORIGIN


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  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 ccatgacgttcctgacgtt 20
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Db     464 CCATGCCGTTCCTGACCTT 482


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Job time: 19241 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 21:08:04 ; Search time 75.06 Seconds
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Title: US-09-369-941-2
Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	20	100.0	20	5	US-09-303-862-12	Sequence 12, Appl
	3	16.8	84.0	20	4	US-09-133-774-11	Sequence 11, Appl
	4	16.8	84.0	20	5	US-08-386-063-25	Sequence 25, Appl
	5	16.8	84.0	20	5	US-09-303-862-11	Sequence 11, Appl
c	6	16.8	84.0	2470	1	US-07-745-206A-14	Sequence 14, Appl
c	7	16.8	84.0	2470	3	US-08-311-363-14	Sequence 14, Appl
c	8	16.8	84.0	5467	1	US-07-745-206A-12	Sequence 12, Appl
c	9	16.8	84.0	5467	3	US-08-311-363-12	Sequence 12, Appl
c	10	16.8	84.0	7175	2	US-08-455-543A-8	Sequence 8, Appli
c	11	16.8	84.0	7175	3	US-08-193-078B-8	Sequence 8, Appli
c	12	16.8	84.0	7175	3	US-08-223-305C-8	Sequence 8, Appli
c	13	16.8	84.0	7175	3	US-08-149-097D-8	Sequence 8, Appli
c	14	16.8	84.0	7175	5	US-08-949-386-8	Sequence 8, Appli
c	15	16.8	84.0	7175	5	US-08-450-562-8	Sequence 8, Appli
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c	17	16.8	84.0	7362	2	US-08-455-543A-7	Sequence 7, Appli
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c	23	15.8	79.0	8931	5	US-09-028-934-28	Sequence 28, Appl
	24	15.2	76.0	1799	3	US-08-560-398-3	Sequence 3, Appli
	25	14.8	74.0	840	1	US-07-906-983-1	Sequence 1, Appli
	26	14.4	72.0	700	5	US-08-764-563-2	Sequence 2, Appli
	27	14.2	71.0	29	2	US-08-484-557C-8	Sequence 8, Appli
	28	14.2	71.0	29	2	US-08-487-426B-8	Sequence 8, Appli
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c	32	14.2	71.0	355	7	5244792-11	Patent No. 5244792
	33	14.2	71.0	523	3	US-08-628-413-1	Sequence 1, Appli
	34	14.2	71.0	1949	2	US-08-760-335A-1	Sequence 1, Appli
c	35	14.2	71.0	1979	2	US-08-392-828C-3	Sequence 3, Appli
c	36	14.2	71.0	1979	5	US-09-330-945-3	Sequence 3, Appli
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	38	14.2	71.0	8140	1	US-08-297-294A-1	Sequence 1, Appli
	39	14.2	71.0	50341	2	US-08-247-901C-1	Sequence 1, Appli
	40	14.2	71.0	50341	4	US-09-075-904-1	Sequence 1, Appli
c	41	13.8	69.0	15239	2	US-08-390-878-17	Sequence 17, Appl
	42	13.6	68.0	20	1	US-08-436-714-7	Sequence 7, Appli
	43	13.6	68.0	20	1	US-08-442-705-7	Sequence 7, Appli
	44	13.6	68.0	20	2	US-08-332-829-7	Sequence 7, Appli
	45	13.6	68.0	20	5	US-08-386-063-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-133-774-12
; Sequence 12, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Hear
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-12

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Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-303-862-12
; Sequence 12, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Hear
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/303,862

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;  CURRENT FILING DATE: 1999-05-03
;  EARLIER APPLICATION NUMBER: 09/133,774
;  EARLIER FILING DATE: 1998-08-12
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Chlamydia trachomatis
;    FEATURE:
;    OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
;    OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
;    OTHER INFORMATION: Chlamydia trachomatis.
US-09-303-862-12


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RESULT   3
US-09-133-774-11
; Sequence 11, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
;  APPLICANT: Bachmaier, Kurt
;  APPLICANT: Hessel, Andrew J.
;  APPLICANT: Neu M.D., Nikolaus
;  APPLICANT: Penninger, Josef M.
;  TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
;  TITLE OF INVENTION: Disease
;  FILE REFERENCE: A-536
;  CURRENT APPLICATION NUMBER: US/09/133,774B
;  CURRENT FILING DATE: 1998-08-12
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Chlamydia trachomatis
;    FEATURE:
;    OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
;    OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
;    OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-11


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RESULT   4
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; Sequence 25, Application US/08386063
; Patent No. 6008200
;  GENERAL INFORMATION:
;    APPLICANT:  Arthur M. Krieg, M.D.
;    TITLE OF INVENTION:  IMMUNOMODULATORY OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/386,063
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ARNOLD, BETH E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIZ-013CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-386-063-25


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 20;
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  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT   5
US-09-303-862-11
; Sequence 11, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
;  APPLICANT: Bachmaier, Kurt
;  APPLICANT: Hessel, Andrew J.
;  APPLICANT: Neu M.D., Nikolaus
;  APPLICANT: Penninger, Josef M.
;  TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Hear
;  TITLE OF INVENTION: Disease
;  FILE REFERENCE: A-536
;  CURRENT APPLICATION NUMBER: US/09/303,862
;  CURRENT FILING DATE: 1999-05-03
;  EARLIER APPLICATION NUMBER: 09/133,774
;  EARLIER FILING DATE: 1998-08-12
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Chlamydia trachomatis
;    FEATURE:
;    OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
;    OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
;    OTHER INFORMATION: Chlamydia trachomatis.
US-09-303-862-11


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity  90.0%;  Pred. No. 3.5;
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Db      1 tccatgacgttcctgatgct 20


RESULT   6
US-07-745-206A-14/c
; Sequence 14, Application US/07745206A
; Patent No. 5429921
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Feldman, Daniel
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 S. LaSalle
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/745,206A
;      FILING DATE:  19910815
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feder, Scott B
;      REFERENCE/DOCKET NUMBER:  51504
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-372-7842
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2470 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2469
US-07-745-206A-14


  Query Match             84.0%;  Score 16.8;  DB 1;  Length 2470;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||  | ||||
Db    509 TCCATGACGTTCCAGCCGTT 490


RESULT   7
US-08-311-363-14/c
; Sequence 14, Application US/08311363
; Patent No. 5876958
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,363
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-51506
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2470 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2469
US-08-311-363-14


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 2470;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||  | ||||
Db    509 TCCATGACGTTCCAGCCGTT 490


RESULT   8
US-07-745-206A-12/c
; Sequence 12, Application US/07745206A
; Patent No. 5429921
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Feldman, Daniel
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 S. LaSalle
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/07/745,206A
;      FILING DATE:  19910815
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feder, Scott B
;      REFERENCE/DOCKET NUMBER:  51504
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-372-7842
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5467 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(144..3164, 3168..3245, 3249..3386, 3390
;      LOCATION:  ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
;      LOCATION:  ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
;      LOCATION:  ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
;      LOCATION:  ..5096, 5100..5306, 5310..5366, 5370..5465)
US-07-745-206A-12


  Query Match             84.0%;  Score 16.8;  DB 1;  Length 5467;
  Best Local Similarity   90.0%;  Pred. No. 7.3;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||||  | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633


RESULT   9
US-08-311-363-12/c
; Sequence 12, Application US/08311363
; Patent No. 5876958
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  Human Calcium Channel Compositions and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/311,363
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-51506
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5467 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(144..3164, 3168..3245, 3249..3386, 3390
;      LOCATION:  ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
;      LOCATION:  ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
;      LOCATION:  ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
;      LOCATION:  ..5096, 5100..5306, 5310..5366, 5370..5465)
US-08-311-363-12


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 5467;
  Best Local Similarity   90.0%;  Pred. No. 7.3;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||||  | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633


RESULT  10
US-08-455-543A-8/c
; Sequence 8, Application US/08455543A
; Patent No. 5792846
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,543A
;      FILING DATE:  May 31, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/223,305
;      FILING DATE:  April 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  April 10, 1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/482,384
;      FILING DATE:  20-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/603,751
;      FILING DATE:  04-APR-1989
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-52517
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-455-543A-8


  Query Match             84.0%;  Score 16.8;  DB 2;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||| | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


RESULT  11
US-08-193-078B-8/c
; Sequence 8, Application US/08193078B
; Patent No. 5846757
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWN, MARTIN, HALLER & McCLAIN
;      STREET:  1660 UNION STREET
;      CITY:  SAN DIEGO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/193,078B
;      FILING DATE:  07-FEB-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-53607
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-193-078B-8


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||| | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


RESULT  12
US-08-223-305C-8/c
; Sequence 8, Application US/08223305C
; Patent No. 5851824
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/223,305C
;      FILING DATE:  April 4, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  April 10, 1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
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;       FILING DATE:  15-AUG-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/620,250
;       FILING DATE:  30-NOV-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/482,384
;       FILING DATE:  20-FEB-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/603,751
;       FILING DATE:  04-APR-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US89/01408
;       FILING DATE:  04-APR-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/176,899
;       FILING DATE:  04-APR-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L.
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  52516  (P519739)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619)238-0999
;       TELEFAX:  (619)238-0062
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7175 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  144..6857
;     FEATURE:
;       NAME/KEY:  5'UTR
;       LOCATION:  1..143
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  6855..7175
US-08-223-305C-8


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||| | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633


RESULT  13
US-08-149-097D-8/c
; Sequence 8, Application US/08149097D
; Patent No. 5874236
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/149,097D
;      FILING DATE:  05-NOV-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US92/06903
;      FILING DATE:  14-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/914,231
;      FILING DATE:  13-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/482,384
;      FILING DATE:  20-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/603,751
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-55038
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-149-097D-8


  Query Match             84.0%;  Score 16.8;  DB 3;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||| | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633
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RESULT 14
US-08-949-386-8/c
; Sequence 8, Application US/08949386
; Patent No. 6090623
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Gillespie, Alison
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/949,386
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,012
;      FILING DATE:  11-AUG-1994
;      APPLICATION NUMBER:  08/149,097
;      FILING DATE:  5-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  519808
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-949-386-8


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatgacgttcctgacgtt 20
           |||||||||||||  | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633


RESULT 15
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US-08-450-562-8/c
; Sequence 8, Application US/08450562
; Patent No. 6096514
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Gillespie, Alison
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,562
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/404,950
;      FILING DATE:  13-MAR-1995
;      APPLICATION NUMBER:  08/336,257
;      FILING DATE:  7-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/314,083
;      FILING DATE:  28-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/311,363
;      FILING DATE:  23-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/290,012
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/223,305
;      FILING DATE:  4-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/193,078
;      FILING DATE:  07-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/149,097
;      FILING DATE:  5-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/914,231
;      FILING DATE:  13-JULY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06903
;      FILING DATE:  14-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/603,751
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;      FILING DATE:  08-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/482,384
;      FILING DATE:  02-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-519812
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7175 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  144..6857
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..143
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  6855..7175
US-08-450-562-8


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 7.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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           |||||||||||| | ||||
Db     652 TCCATGACGTTCCAGCCGTT 633



Search completed: December  4, 2000, 21:08:06
Job time: 16804 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 21:09:55 ; Search time 99.31 Seconds
(without alignments)
75.655 Million cell updates/sec

Title: US-09-369-941-2
Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	19	V60950	Unmethylated cytos
	2	20	100.0	20	19	V47683	Unmethylated CpG d
	3	20	100.0	20	19	V27667	Immunostimulatory
	4	20	100.0	20	20	Z31943	CpG adjuvant oligo
	5	20	100.0	20	20	Z41946	IL-12 secretion in
	6	20	100.0	20	20	Z41949	IL-12 secretion in
	7	20	100.0	20	20	Z28191	Chlamydia trachoma
	8	20	100.0	20	20	X78802	HPV fusion protein
	9	20	100.0	20	20	X88536	Cytosine-guanosine
	10	20	100.0	20	20	V74237	CpG-N motif S-ODN
	11	20	100.0	20	20	V74242	CpG-N motif O-ODN
	12	20	100.0	20	20	V74244	CpG-N motif SOS-OD
	13	20	100.0	20	21	Z99004	CpG motif for immu
	14	20	100.0	20	21	Z99174	Inflammatory cardi
	15	20	100.0	20	21	Z61010	Nucleotide sequenc
	16	20	100.0	20	21	Z61012	Nucleotide sequenc
	17	20	100.0	20	21	Z47601	Murine immune syst
	18	20	100.0	20	21	Z47885	Immunostimulatory
	19	20	100.0	20	21	Z47887	Immunostimulatory
	20	20	100.0	20	21	Z48022	Immune remodeling
	21	20	100.0	20	21	Z48025	Immune remodeling
c	22	20	100.0	44	20	V83723	Murine-specific Cp
	23	20	100.0	44	20	V83722	Murine-specific Cp
	24	20	100.0	44	20	V83726	CpG-optimised gene
	25	17	85.0	17	19	V52557	Unmethylated CpG d
	26	17	85.0	17	19	V27731	Immunostimulatory
	27	17	85.0	17	20	Z41916	IL-12 secretion in
	28	17	85.0	17	21	Z60984	Nucleotide sequenc
	29	17	85.0	17	21	Z47653	Parasitic infectio
	30	17	85.0	17	21	Z47859	Immunostimulatory
	31	17	85.0	17	21	Z47992	Immune remodeling
	32	16.8	84.0	20	18	T88792	Synthetic phosphor
	33	16.8	84.0	20	19	V52567	Unmethylated CpG d
	34	16.8	84.0	20	19	V45995	Immune adjuvant Cp
	35	16.8	84.0	20	19	V45996	Immune adjuvant Cp
	36	16.8	84.0	20	19	V27708	Immunostimulatory
	37	16.8	84.0	20	19	V27700	Immunostimulatory
	38	16.8	84.0	20	19	V27651	Immunostimulatory
	39	16.8	84.0	20	19	V27638	Immunostimulatory
	40	16.8	84.0	20	20	Z41879	IL-12 secretion in
	41	16.8	84.0	20	20	Z41919	IL-12 secretion in
	42	16.8	84.0	20	20	Z41930	IL-12 secretion in
	43	16.8	84.0	20	20	Z28190	Chlamydia trachoma
	44	16.8	84.0	20	20	V72500	CpG motif containi
	45	16.8	84.0	20	20	V74261	CpG-N motif oligon

ALIGNMENTS

RESULT 1
V60950
ID V60950 standard; DNA; 20 BP.
XX
AC V60950;
XX
DT 14-DEC-1998 (first entry)
XX
DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
XX
KW ss; unmethylated CpG dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.
XX
OS Synthetic.
XX
PN WO9840100-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US04703.
XX
PR 10-MAR-1997; 97US-0040376.
XX
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Davis HL, Krieg AM, Schorr J;
XX
DR WPI; 1998-520792/44.
XX
PT Use of oligonucleotides containing an unmethylated CpG dinucleotide
PT - useful as, e.g. adjuvant with antigen, or nucleic acid encoding
PT antigen for inducing immune response in subject
XX

PS Claim 14; Page 35; 67pp; English.
XX
CC Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
CC affect the immune response in a subject by activating natural killer
CC cells or redirecting a subject's immune response from a Th2 to a Th1
CC response by inducing monocytic and other cells to produce Th1 cytokines.
CC These nucleic acids containing at least 1 unmethylated CpG can be used as
CC an adjuvant, specifically to induce an immune response against an
CC antigenic protein, and are used particularly for virally mediated
CC disorders, e.g. hepatitis B virus infection.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 2
V47683
ID V47683 standard; DNA; 20 BP.
XX
AC V47683;
XX
DT 20-NOV-1998 (first entry)
XX
DE Unmethylated CpG dinucleotide 1826.
XX
KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.
XX
OS Synthetic.
XX
PN WO9837919-A1.
XX
PD 03-SEP-1998.
XX
PF 25-FEB-1998; 98WO-US03678.
XX
PR 28-FEB-1997; 97US-0039405.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Schwartz DA;
XX
DR WPI; 1998-480941/41.
XX
PT Use of nucleic acids containing an unmethylated CpG - for treating a
PT subject having or at risk of having an acute decrement in air flow
PT or inhibiting an inflammatory response
XX
PS Claim 35; Page 27; 65pp; English.
XX
CC This sequence represents an unmethylated CpG dinucleotide, and can be
CC used in the method of the invention. The method is for treating a subject
CC having, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with
CC Gram-positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 3
V27667
ID V27667 standard; DNA; 20 BP.
XX
AC V27667;
XX
DT 01-OCT-1998 (first entry)
XX
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
PN WO9818810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19791.
XX
PR 30-OCT-1996; 96US-0738652.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Kline JN, Krieg AM;
XX
DR WPI; 1998-272127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at
PT least one unmethylated CpG dinucleotide, used for treating e.g.
PT tumours, infections or autoimmune disease
XX
PS Claim 35; Page 84; 109pp; English.
XX
CC V27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC of the invention. The ODNs contain at least one unmethylated CpG
CC dinucleotide, and have the formula:
CC 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
CC CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is
CC any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2
CC does not contain a CCGG tetramer or more than one CCG or CGG trimer OR
CC 5' NX1X2CGX3X4N 3', where at least one nucleotide separates consecutive
CC CpGs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA, X3and X4
CC are selected from TpT or CpT, N is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCGG tetramer
CC or more than one CCG or CGG trimer.
CC The ODNs activate lymphocytes in a subject and redirect a subject's
CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells and
CC other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune diseases, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a
CC human.

```
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 19;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20


RESULT   4
Z31943
ID   Z31943 standard; DNA; 20 BP.
XX
AC   Z31943;
XX
DT   26-JAN-2000  (first entry)
XX
DE   CpG adjuvant oligo 1001.
XX
KW   CpG adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;
KW   antigen; infection; allergy; cancer; therapy; ss.
XX
OS   Synthetic.
XX
PN   WO9952549-A1.
XX
PD   21-OCT-1999.
XX
PF   29-MAR-1999;   99WO-EP02278.
XX
PR   09-APR-1998;   98GB-0007805.
PR   25-SEP-1998;   98GB-0020956.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Friede M,  Hermand P;
XX
DR   WPI; 1999-620290/53.
XX
PT   Vaccine to protect against infections, allergy and cancer  -
XX
PS   Claim 16; Page 32; 52pp; English.
XX
CC   This sequence represents a CpG adjuvant that can be used in the vaccine
CC   composition of the invention. The vaccine comprises a polyoxyethylene
CC   ether or ester (I), not in the form of a vesicle, pharmaceutically
CC   acceptable excipient and an antigen (Ag) or antigenic composition. The
CC   vaccine can be used to treat or prevent infections (by bacteria, viruses
CC   or other parasites), allergy and cancer. (I), which are safe, easy to
CC   sterilize and simple to administer, are powerful vaccine adjuvants, able
CC   to induce a systemic immune response when administered (non-invasively)
CC   to the mucosa. The response is at least as good as that from conventional
CC   systemic injection. (I) are effective at low concentration, have low
CC   reactogenicity and are well tolerated.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20


RESULT   5
Z41946
ID   Z41946 standard; DNA; 20 BP.
XX
AC   Z41946;
XX
DT   24-JAN-2000  (first entry)
XX
DE   IL-12 secretion inducing CpG oligonucleotide 91.
XX
KW   CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KW   human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW   neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW   antigen presenting cell; infection; allergic disease.
XX
OS   Synthetic.
XX
PN   WO9951259-A2.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999;   99WO-US07335.
XX
PR   03-APR-1998;   98US-0080729.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Krieg AM,  Weiner G;
XX
DR   WPI; 1999-620169/53.
XX
PT   Novel synergistic combinations of immunostimulatory oligonucleotides
PT   and immunopotentiating cytokines are useful for stimulating the immune
PT   system  -
XX
PS   Example 8; Page 88; 91pp; English.
XX
CC   Sequences Z41856-Z41949 are phosphorothioate CpG oligonucleotides which
CC   are used in the invention to induce interleukin-12 (IL-12) secretion
CC   from human PBMC. The invention comprises stimulating an immune response
CC   in a subject comprising administering to a subject exposed to an antigen,
CC   an immunopotentiating cytokine and an immunostimulatory CpG
CC   oligonucleotide to induce a synergistic antigen specific immune response.
CC   The methods are useful for treating cancer by stimulating an antigen
CC   specific immune response against a cancer antigen. The methods can also
CC   be used to treat neoplastic disorders in humans, including but not
CC   limited to: sarcoma, carcinoma, fibroma, Lymphoma, melanoma,
CC   neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC   for treating infectious diseases, e.g. viral diseases such as HIV,
CC   bacterial diseases, and fungal diseases. The methods may also be used to
CC   treat allergic diseases, e.g. asthma. The methods and compositions may
CC   also be applied to treat cancer and tumours in non human subjects,
CC   e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC   be treated and include leukaemia, haemangiopericytoma and bovine ocular
CC   neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC   caused by the bacterium Corynebacterium pseudotuberculosis, and
CC   contagious lung tumour of sheep caused by jaagsiekte may also be treated.
CC   CpG oligonucleotides can be useful in activating B cells, NK cells, and
CC   antigen presenting cells, such as monocytes and macrophages. CpG
CC   oligonucleotides enhance antibody dependent cellular cytotoxicity and can
CC   be used as an adjuvant in conjunction with tumour antigens to protect
CC   against a tumour challenge.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20
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```
RESULT   6
Z41949
ID   Z41949 standard; DNA; 20 BP.
XX
AC   Z41949;
XX
DT   24-JAN-2000  (first entry)
XX
DE   IL-12 secretion inducing CpG oligonucleotide 94.
XX
KW   CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KW   human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW   neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW   antigen presenting cell; infection; allergic disease.
XX
OS   Synthetic.
XX
PN   WO9951259-A2.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999;   99WO-US07335.
XX
PR   03-APR-1998;   98US-0080729.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Krieg AM,  Weiner G;
XX
DR   WPI; 1999-620169/53.
XX
PT   Novel synergistic combinations of immunostimulatory oligonucleotides
PT   and immunopotentiating cytokines are useful for stimulating the immune
PT   system  -
XX
PS   Example 8; Page 89; 91pp; English.
XX
CC   Sequences Z41856-Z41949 are phosphorothioate CpG oligonucleotides which
CC   are used in the invention to induce interleukin-12 (IL-12) secretion
CC   from human PBMC. The invention comprises stimulating an immune response
CC   in a subject comprising administering to a subject exposed to an antigen,
CC   an immunopotentiating cytokine and an immunostimulatory CpG
CC   oligonucleotide to induce a synergistic antigen specific immune response.
CC   The methods are useful for treating cancer by stimulating an antigen
CC   specific immune response against a cancer antigen. The methods can also
CC   be used to treat neoplastic disorders in humans, including but not
CC   limited to: sarcoma, carcinoma, fibroma, Lymphoma, melanoma,
CC   neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC   for treating infectious diseases, e.g. viral diseases such as HIV,
CC   bacterial diseases, and fungal diseases. The methods may also be used to
CC   treat allergic diseases, e.g. asthma. The methods and compositions may
CC   also be applied to treat cancer and tumours in non human subjects,
CC   e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC   be treated and include leukaemia, haemangiopericytoma and bovine ocular
CC   neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC   caused by the bacterium Corynebacterium pseudotuberculosis, and
CC   contagious lung tumour of sheep caused by jaagsiekte may also be treated.
CC   CpG oligonucleotides can be useful in activating B cells, NK cells, and
CC   antigen presenting cells, such as monocytes and macrophages. CpG
CC   oligonucleotides enhance antibody dependent cellular cytotoxicity and can
CC   be used as an adjuvant in conjunction with tumour antigens to protect
CC   against a tumour challenge.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20
```

```
RESULT   7
Z28191
ID   Z28191 standard; DNA; 20 BP.
XX
AC   Z28191;
XX
DT   20-DEC-1999  (first entry)
XX
DE   Chlamydia trachomatis outer membrane protein gene-derived CpG oligo 4.
XX
KW   Heart disease; inflammatory; autoimmune; cardiomyopathy; adjuvant;
KW   CpG motif; vaccine; ds.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = phosphorothioate linkage"
XX
PN   US5962636-A.
XX
PD   05-OCT-1999.
XX
PF   12-AUG-1998;   98US-0133774.
XX
PR   12-AUG-1998;   98US-0133774.
XX
PA   (AMGE-) AMGEN CANADA INC.
XX
PI   Bachmaier K,  Hessel AJ,  Penninger JM,  Neu N;
XX
DR   WPI; 1999-589735/50.
XX
PT   Peptides that induce or suppress inflammatory cardiomyopathy  -
XX
PS   Example 2; Column 25; 17pp; English.
XX
CC   This sequence represents DNA encoding Chlamydia trachomatis 60 kD outer
CC   membrane protein (OMP) gene-derived CpG oligonucleotide 4. This
CC   oligonucleotide contains a CpG motif. It was tested for its ability to
CC   act as an adjuvant for the M7A-alpha peptide (Y42723), which can induce
CC   inflammatory cardiomyopathy (ICM) in mice. It was found to act as a
CC   potent immunostimulator, whereas a oligonucleotide from the same
CC   source which did not contain a CpG motif (Z28193) was hardly effective as
CC   an adjuvant. Inflammatory cardiomyopathy peptides (Y42723, Y42725-Y42731)
CC   can be used with such an adjuvant and an excipient in a vaccine for
CC   decreasing ICM.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20
```

```
RESULT   8
X78802
ID   X78802 standard; DNA; 20 BP.
XX
AC   X78802;
XX
DT   06-SEP-1999  (first entry)
XX
```

DE HPV fusion protein CpG oligonucleotide 1.
XX
KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW immunological fusion partner; CpG oligonucleotide; immune response;
KW HPV antigen; prevention; treatment; primer; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO9933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP08563.
XX
PR 24-DEC-1997; 97GB-0027262.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Gerard CMG;
XX
DR WPI; 1999-405485/34.
XX
PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV
XX
PS Claim 11; Page 36; 62pp; English.
XX
CC X78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in Y25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used
CC for preventing or treating HPV induced tumours. This sequence represents
CC a CpG oligonucleotide which is used in the method of the invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 9
X88536
ID X88536 standard; DNA; 20 BP.
XX
AC X88536;
XX
DT 10-SEP-1999 (first entry)
XX
DE Cytosine-guanosine dinucleotide motif oligonucleotide #3.
XX
KW Cytosine-guanosine dinucleotide motif; CpG; immunomodulation;
KW unmethylated; vaccine; immunostimulation; immune response;
KW T-independent type 1 antigen; T-independent type 2 antigen;
KW polysaccharide conjugate antigen; ss.
XX
OS Synthetic.
XX
PN WO9933488-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP08562.
XX
PR 24-DEC-1997; 97GB-0027262.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Laferriere CAJ, Prieels J;
XX
DR WPI; 1999-405369/34.
XX
PT A vaccine composition for inducing a immune response to
PT T-independent type 1 or type 2 antigen or polysaccharide conjugate
PT antigen
XX
PS Claim 6; Page 31; 35pp; English.
XX
CC The present invention describes a formulation (A) comprising a
CC cytosine-guanosine dinucleotide motif (CpG) oligonucleotide and
CC T-independent type 1 or type 2 antigens or polysaccharide conjugate
CC antigen. The present sequence represent a specifically claimed CpG
CC oligonucleotide. A vaccine composition comprising the formulation is
CC used for inducing a immune response to T-independent type 1 or type 2
CC antigen or polysaccharide conjugate antigen. The use of
CC immunostimulatory CpG oligonucleotide acts as an adjuvant to
CC pneumococcal polysaccharides.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 10
V74237
ID V74237 standard; DNA; 20 BP.
XX
AC V74237;
XX
DT 15-MAR-1999 (first entry)
XX
DE CpG-N motif S-ODN 1826 DNA.
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10408.
XX
PR 20-MAY-1997; 97US-0047233.
PR 20-MAY-1997; 97US-0047209.
XX
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA-) UNIV IOWA RES FOUND.
XX
PI Davis HL, Krieg AM, Schorr J, Wu T;
XX
DR WPI; 1999-059712/05.
XX
PT Use of neutralising CpG and stimulating CpG motifs in DNA vectors -
PT for enhancing the immunostimulatory effect of an antigen or
PT enhancing the expression of a therapeutic polypeptide
XX

PS Example 1; Page 64; 109pp; English.
XX
CC V74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
CC method for enhancing the immunostimulatory effect of an antigen encoded
CC by nucleic acid contained in a nucleic acid construct. The method
CC involves determining the CpG-N and CpG-S motifs present in the construct,
CC removing neutralising CpG (CpG-N) motifs and optionally inserting
CC stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
CC nucleic acid construct having enhanced immunostimulatory efficacy. The
CC method can be used for immunisation against viral antigens, e.g. from
CC hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
CC parasite. They can also be used for expression of a therapeutic
CC polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
CC apoptotic proteins, interferons, hormones, clotting factors, ligands and
CC receptors.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 11
V74242
ID V74242 standard; DNA; 20 BP.
XX
AC V74242;
XX
DT 15-MAR-1999 (first entry)
XX
DE CpG-N motif O-ODN 2061 DNA.
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10408.
XX
PR 20-MAY-1997; 97US-0047233.
PR 20-MAY-1997; 97US-0047209.
XX
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA-) UNIV IOWA RES FOUND.
XX
PI Davis HL, Krieg AM, Schorr J, Wu T;
XX
DR WPI; 1999-059712/05.
XX
PT Use of neutralising CpG and stimulating CpG motifs in DNA vectors -
PT for enhancing the immunostimulatory effect of an antigen or
PT enhancing the expression of a therapeutic polypeptide
XX
PS Example 1; Page 64; 109pp; English.
XX
CC V74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
CC method for enhancing the immunostimulatory effect of an antigen encoded
CC by nucleic acid contained in a nucleic acid construct. The method
CC involves determining the CpG-N and CpG-S motifs present in the construct,
CC removing neutralising CpG (CpG-N) motifs and optionally inserting
CC stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
CC nucleic acid construct having enhanced immunostimulatory efficacy. The
CC method can be used for immunisation against viral antigens, e.g. from
CC hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
CC parasite. They can also be used for expression of a therapeutic
CC polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
CC apoptotic proteins, interferons, hormones, clotting factors, ligands and
CC receptors.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

RESULT 12
V74244
ID V74244 standard; DNA; 20 BP.
XX
AC V74244;
XX
DT 15-MAR-1999 (first entry)
XX
DE CpG-N motif SOS-ODN 1980 DNA.
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10408.
XX
PR 20-MAY-1997; 97US-0047233.
PR 20-MAY-1997; 97US-0047209.
XX
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA-) UNIV IOWA RES FOUND.
XX
PI Davis HL, Krieg AM, Schorr J, Wu T;
XX
DR WPI; 1999-059712/05.
XX
PT Use of neutralising CpG and stimulating CpG motifs in DNA vectors -
PT for enhancing the immunostimulatory effect of an antigen or
PT enhancing the expression of a therapeutic polypeptide
XX
PS Example 1; Page 64; 109pp; English.
XX
CC V74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
CC method for enhancing the immunostimulatory effect of an antigen encoded
CC by nucleic acid contained in a nucleic acid construct. The method
CC involves determining the CpG-N and CpG-S motifs present in the construct,
CC removing neutralising CpG (CpG-N) motifs and optionally inserting
CC stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
CC nucleic acid construct having enhanced immunostimulatory efficacy. The
CC method can be used for immunisation against viral antigens, e.g. from
CC hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
CC parasite. They can also be used for expression of a therapeutic
CC polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
CC apoptotic proteins, interferons, hormones, clotting factors, ligands and

```
CC   receptors.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20


RESULT  13
Z99004
ID   Z99004 standard; DNA; 20 BP.
XX
AC   Z99004;
XX
DT   21-JUN-2000  (first entry)
XX
DE   CpG motif for immunostimulatory oligonucleotide 1826.
XX
KW   Immunoprotective; vaccine; antigen; saponin adjuvant; immune response;
KW   immunostimulatory oligonucleotide; unmethylated CpG dinucleotide;
KW   mammal; human; animal; ss.
XX
OS   Synthetic.
XX
PN   WO200009159-A1.
XX
PD   24-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US17956.
XX
PR   10-AUG-1998;   98US-0095913.
PR   08-APR-1999;   99US-0128608.
XX
PA   (AQUI-) AQUILA BIOPHARMACEUTICALS INC.
XX
PI   Kensil CA;
XX
DR   WPI; 2000-224181/19.
XX
PT   A vaccine composition comprising an antigen, saponin adjuvant and
PT   immunostimulatory CpG oligonucleotide, useful for stimulating immunity
PT   and increasing immune responses  -
XX
PS   Claim 10; Page 19; 38pp; English.
XX
CC   The invention relates to a vaccine composition comprising an antigen,
CC   a saponin adjuvant and an immunostimulatory oligonucleotide. The
CC   immunostimulatory oligonucleotide preferably comprises at least one
CC   unmethylated CpG dinucleotide. This sequence represents an example of
CC   the immunostimulatory oligonucleotide. The vaccine composition increases
CC   the immune response to the antigen when administered to a mammal,
CC   especially a human or animal. It further stimulates immunity and
CC   especially enhances antibody production to the antigen, preferably in a
CC   positive synergistic manner. It further enhances cell-mediated immunity.
CC   The immune adjuvant in particular can be used to increase the immune
CC   response to an antigen in an individual or a test system.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20


RESULT  14
Z99174
ID   Z99174 standard; DNA; 20 BP.
XX
AC   Z99174;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Inflammatory cardiomyopathy immunostimulatory oligonucleotide #3.
XX
KW   Cardiant; murine alpha myosin heavy chain; inflammatory myocarditis;
KW   autoimmune inflammatory cardiomyopathy; Chlamydia; antibody; vaccine;
KW   hybridization probe; immunostimulatory; ss.
XX
OS   Synthetic.
XX
PN   US6034230-A.
XX
PD   07-MAR-2000.
XX
PF   03-MAY-1999;   99US-0303862.
XX
PR   12-AUG-1998;   98US-0133774.
XX
PA   (AMGE-) AMGEN CANADA INC.
XX
PI   Neu N,  Penninger JM,  Bachmaier K,  Hessel AJ;
XX
DR   WPI; 2000-255712/22.
XX
PT   DNA molecules encoding novel myocardial peptides used for inhibiting
PT   and inducing inflammatory cardiomyopathy in vivo  -
XX
PS   Disclosure; Column 17; 17pp; English.
XX
CC   The invention relates to the isolation of sequences coding for peptide
CC   sequences derived from bacteria and viruses which may cause inflammatory
CC   cardiomyopathy. The peptide sequences are searched based on the sequence
CC   of the M7A peptides derived from the murine alpha myosin heavy chain
CC   polypeptide. The consensus sequence of the murine M7A-alpha/beta peptides
CC   (Y83813) was used to search the PIR public database for similar bacterial
CC   and viral sequences able to cause inflammatory cardiomyopathy. The screen
CC   isolated the peptides Y83814-Y83819 and their corresponding coding
CC   sequences Z99164-Z99169. The peptides encoded by the DNAs are used, alone
CC   or in conjunction with other therapeutics, for inducing or inhibiting
CC   inflammatory cardiomyopathy in vivo, where the cardiomyopathy is
CC   autoimmune inflammatory cardiomyopathy, and inflammatory cardiomyopathy
CC   caused by Chlamydia or other bacterial or viral infections that cause
CC   inflammatory cardiomyopathy. The oligonucleotides Z99172-Z99176 were
CC   shown to increase the immunogenicity of the immunostimulatory peptides
CC   when injected simultaneously. The peptides may also be used for
CC   increasing inflammatory myocarditis in a mammal. Antibodies against the
CC   peptides and the peptides themselves are used for measuring the risk of
CC   inflammatory cardiomyopathy in a mammal. The peptides may also be used
CC   in vaccines. Nucleic acids encoding the peptides may be used as
CC   hybridization probes, e.g. in diagnostic assays to test for the
CC   presence of Chlamydia DNA.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db      1 tccatgacgttcctgacgtt 20


RESULT  15
```

Z61010
ID Z61010 standard; DNA; 20 BP.
XX
AC Z61010;
XX
DT 30-MAY-2000 (first entry)
XX
DE Nucleotide sequence of an immunostimulatory CpG oligonucleotide.
XX
KW Immunostimulatory; stereoisomer; CpG oligonucleotide; Th2; Th1; asthma;
KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;
KW inflammatory disease; inflammatory bowel disease; autoimmune disease;
KW gingivitis; psoriasis; sepsis; ss.
XX
OS Synthetic.
XX
PN WO200006588-A1.
XX
PD 10-FEB-2000.
XX
PF 27-JUL-1999; 99WO-US17100.
XX
PR 27-JUL-1998; 98US-0094370.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
PI Krieg AM;
XX
DR WPI; 2000-195254/17.
XX
PT Immunostimulatory and immunoinhibitory stereoisomers of CpG
PT oligonucleotides useful for immunotherapy of cancer -
XX
PS Disclosure; Page 12; 88pp; English.
XX
CC Z60933-Z61015 represent immunostimulatory stereoisomers of CpG
CC oligonucleotides. The sequences are derived from generic nucleic
CC acid sequence, from which immunoinhibitory sequences may also be
CC derived. The immunostimulatory nucleic acids can be co-administered
CC with an antigen to induce an antigen-specific immune response. The
CC immunostimulatory nucleic acids can also be used in methods for
CC redirecting a subject's immune response from a Th2 to a Th1, for
CC treating asthma, for desensitising a subject against the occurrence
CC of an allergic reaction in response to contact with an allergen, for
CC activating an immune cell, especially a lymphocyte or a dendritic cell
CC expressing a cancer antigen or for treating cancer. The immunoinhibitory
CC nucleic acid can be used to prevent an immune response, especially where
CC the immune response in the subject is excessive due to having received
CC an immune stimulating compound. The immunoinhibitory nucleic acid can
CC be used to treat a subject having or at risk of an inflammatory disease,
CC especially inflammatory bowel disease, autoimmune disease, gingivitis,
CC psoriasis and sepsis.
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatgacgttcctgacgtt 20
||||||||||||||||||||
Db 1 tccatgacgttcctgacgtt 20

Search completed: December 4, 2000, 21:09:55
Job time: 16673 sec

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DEFINITION  Sequence 8 from patent US 5846757.
ACCESSION   AR063883
VERSION     AR063883.1  GI:5993191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7175)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Human calcium channel .alpha. .sub.1, .alpha. .sub.2, and .beta.
            subunits and assays using them
  JOURNAL   Patent: US 5846757-A 8 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .7175
                     /organism="unknown"
BASE COUNT     1415 a   2197 c   2168 g   1395 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||| | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


RESULT  15
AR067883/c
LOCUS       AR067883     7175 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 8 from patent US 5851824.
ACCESSION   AR067883
VERSION     AR067883.1  GI:5999105
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7175)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Human calcium channel .alpha.-1C/.alpha.-1D, .alpha.-2, .beta.-1,
            and .gamma.subunits and cells expressing the DNA
  JOURNAL   Patent: US 5851824-A 8 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .7175
                     /organism="unknown"
BASE COUNT     1415 a   2197 c   2168 g   1395 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 7175;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||| | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


Search completed: December  4, 2000, 20:47:28
Job time: 18088 sec
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     source          1. .5467
                     /organism="unknown"
BASE COUNT     1105 a   1598 c   1659 g   1105 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 5467;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||  | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


RESULT  12
D86600/c
LOCUS       D86600       7113 bp    mRNA            INV       08-MAR-2000
DEFINITION  Loligo bleekeri mRNA for voltage-dependent calcium channel,
            complete cds.
ACCESSION   D86600
VERSION     D86600.2  GI:7209875
KEYWORDS    voltage-dependent calcium channel; neural calcium channel
            alpha1-subunit.
SOURCE      Loligo bleekeri cDNA to mRNA.
  ORGANISM  Loligo bleekeri
            Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
            Myopsida; Loliginidae; Loligo.
REFERENCE   1  (sites)
  AUTHORS   Kimura,T., Shouno,O., Hirota,K., Saito,T., Matsumoto,G. and Sato,C.
  TITLE     Molecular cloning and characterization of a putative neural calcium
            channel alpha1-subunit from squid optic lobe
  JOURNAL   Biochem. Biophys. Res. Commun. 230 (1), 147-154 (1997)
  MEDLINE   97148591
REFERENCE   2  (bases 1 to 7113)
  AUTHORS   Kimura,T., Shouno,O., Sato,C., Hirota,K., Hanyu,Y., Saito,T. and
            Matsumoto,G.
  TITLE     Primary structure of a putative calcium channel alpha1-subunit from
            squid optic lobe
  JOURNAL   Unpublished (1996)
REFERENCE   3  (bases 1 to 7113)
  AUTHORS   Kimura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-1996) to the DDBJ/EMBL/GenBank databases. Tadashi
            Kimura, Electrotechnical Laboratory, Supermolecular Science
            Division; 1-1-4 Umezono, Tsukuba, Ibaraki 305, Japan
            (E-mail:eveda@etl.go.jp, Tel:029854508066616)
COMMENT     On Mar 8, 2000 this sequence version replaced gi:1817549.
            Sequence updated (27-Nov-1996) by: Tadashi Kimura
            Sequence updated (06-Mar-2000).
FEATURES             Location/Qualifiers
     source          1. .7113
                     /organism="Loligo bleekeri"
                     /db_xref="taxon:6617"
     CDS             329. .6919
                     /note="neural calcium channel alpha1-subunit"
                     /codon_start=1
                     /product="voltage-dependent calcium channel"
                     /protein_id="BAA13136.2"
                     /db_xref="GI:7209876"
                     /translation="MNTFSADTGGRDDGDYTHDGSLQFVAKKAATVSLPGMGSSTNRS
                     LFIFSEENFIRKYAKIIIEWGPFEYMVLLTIIANCIVLALEEHLPNEDKTPLAVQLEA
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                     RTLRAVRVLRPLKLVSGIPSLQVVLKSIIRAMAPLLQVCLLVLFAIVIFAIIGLEFYT
                     GAFHKACFIKPNDDSEDNIEYGDEDTIRPCANEGSGYHCRANIAKCRFNWAGPNYGIT
                     SFDNMGFAMLTVFQCVTMEGWTQVLYYTDDAVGDAYNWIYFVPLIVLGSFFMLNLVLG
                     VLSGEFAKERERVENRRAFLKLRRQQQIERELNGYLEWICKAEEVILDEERKKDDGTI
                     SDEDKLRIIEGALGFNARRLAAQKVKKMKENKELTIGDEDNDGDLLSGINVGGSFGRG
                     LKNRKAHGRCAGFWRAEKHLRFTIRKCVKTQGFYWFVIILVFLNTLCVASEHYGQAEW
                     HTEFLYVMEFAFLALFMSEMLIKMYGLGVRLYFQSSFNIFDCVVILVSIIEVIWSAIK
                     DGSSFGISTLRALRLLRMFKVTRYWSSLRNLVVSLLSSMRSIVSLLFLLFLFILIFAL
                     LGMQLFGGMMNFEEGRPPGHFDTFPIALLTVFQILTGEDWNEVMYSGIRARGGIAGGG
                     MLYCSYFIILVLFGNYTLLNVFLAIAVDNLANAQELTAAEEIQEGVRQEQEAAEKKKL
                     AEEAAEKEKLARMEEIEKDLCPDQFGLTPPQVNICPPSPQNNEDLKTGNFPYNTSRLD
                     SNLNQNNIKEERNKIGADKDLKKDRDPLDNVSLHESNANRNNAQPGSSSNLNIQPQNG
                     NSEEPAFGGPKPMLPYSSMFIFGPTNPVRRFCHFVVNLRYFDLFIMIVICASSIALAA
                     EDPVNDESVNNQILNYFDYVFTGVFTIEMLLKIVDLGIILHPGSYCRDAWNILDATVV
                     ICALVAFAFGDAAGGNLNTIKSLRVLRVLRPLKTINRIPKLKAVFDCVVNSLKNVSNI
                     LIVYLLFQFIFAVIAVQLFKGKFFYCTDMSKSNREECQGQYFDYEDESDKPRVKNREW
                     LRQDFHYDNVMFAMLTLFTVTTGEGWPMVLKNSMDSTSDDMGPKPGYRMEMAIYYVVF
                     FIVFPFFFVNIFVALIIITFQEQGENELVDQDLDKNQKQCIEFSIEAKPSCRYVPKNK
                     NSIKYKIWQVVVSPKFECVVMVLIALNTLVLMMKYYGSPTEYKLLLQNLNLAFSVLFT
                     IECILKLMGFGIGNYFRDRWNMFDFIIVIGSIIDVVTTNVLPSASSFRTGSFRLFRAA
                     RLVKLLRQGYTIRLLLWTFLQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIRLDSKTS
                     INRHNNFRSFFYAVLLLFRCATGESWQQIMLSCLSGRPCDPESKMLDNSCGLDIAYIY
                     FVTFIFLCSFLMLNLFVAVIMDNFDYLTRDTSILGPHHLDEYSRVWAEYDPLASGRVH
                     YTDMYEMLRRMEPPVGFGRNCPYRLACRKLIRMNMPLKEDGTVHFSTTLFALVRESLS
                     IRMSSAEEMDKKDEEMREVIKRVWPVQGKKIVDLLVPPNHELNNGKLTVGKVYGGLLI
                     AENWRAYKASQNQNNSLKTEKKEELFWEDDIKEYRDEEDYREYRDEEDYKDDYQEYQE
                     YQEDCKDYEEDYNQVETLEIESRNKYHSTPLHSPCIAINGQQFQFQQLQYSDSEERPP
                     SIFQRIMGVMRTPSARSSQGIDSEHSDNEMEGGHSIDKSHDKSTWQRSFSFLRRGSSR
                     RRKDSTVQKSETASLQPSEKQDFSWGLRPEHAAHPSAPRPGSGSSRGLNFAQTVPLSP
                     VSPRSPLPSQSPLGSPLASPSMHRRSVSPRRGLDVGFASAVSNIVDQAHSIAEHDRHR
                     KHRAYFHPGKPDDSLSVPTSPQMRGRSRGRHRPPLQQQGQVMGSPLPGPTSRRKEPTF
                     YRSTSLENRSRSPSPNLTPTSTLHQHEYYGSAGLTDRSRSPSPTMTPPRKATRKLPAV
                     PSKPSTLNLAQTRPRENMPRVMPSPTVPQPSKSPGSINFPRLNASPTHIPRVGPTIGQ
                     APPLGRLGRPEPYSPTERNCISKLSPERSRTLPIGQRISNRDFSRGVDLYVSHRSRTF
                     DPRINDRGRYFDDPSLDAHMSDHRSETLPNGFKPKKRKPENLDMRGDGTGGPVRHESD
                     EDDDWC"
BASE COUNT     2146 a   1383 c   1514 g   2070 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 33;  Length 7113;
  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
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Db    747 TCCATGATGTTCCAGACGTT 728


RESULT  13
AR022380/c
LOCUS       AR022380     7175 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 8 from patent US 5792846.
ACCESSION   AR022380
VERSION     AR022380.1  GI:3976442
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7175)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Human calcium channel compositions and methods
  JOURNAL   Patent: US 5792846-A 8 11-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .7175
                     /organism="unknown"
BASE COUNT     1415 a   2197 c   2168 g   1395 t
ORIGIN


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  Best Local Similarity   90.0%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||  | ||||
Db    652 TCCATGACGTTCCAGCCGTT 633


RESULT  14
AR063883/c
LOCUS       AR063883     7175 bp    DNA             PAT       29-SEP-1999
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RESULT   7
A90870
LOCUS       A90870         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 5 from Patent EP0855184.
ACCESSION   A90870
VERSION     A90870.1  GI:6739264
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | |
Db      1 TCCATGACGTTCCTGATGCT 20


RESULT   8
A93512
LOCUS       A93512         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 5 from Patent WO9740163.
ACCESSION   A93512
VERSION     A93512.1  GI:6741731
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Colpan,M. and Schorr,J.
  TITLE     NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
  JOURNAL   Patent: WO 9740163-A 30-OCT-1997;
            COLPAN METIN (DE); SCHORR JOACHIM (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | |
Db      1 TCCATGACGTTCCTGATGCT 20


RESULT   9
A93521
LOCUS       A93521         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 14 from Patent WO9740163.
ACCESSION   A93521
VERSION     A93521.1  GI:6741738
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Colpan,M. and Schorr,J.
  TITLE     NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
  JOURNAL   Patent: WO 9740163-A 30-OCT-1997;
            COLPAN METIN (DE); SCHORR JOACHIM (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | |
Db      1 TCCATGACGTTCCTGATGCT 20


RESULT  10
I12881/c
LOCUS       I12881       2470 bp    DNA             PAT       26-JUL-1995
DEFINITION  Sequence 14 from patent US 5429921.
ACCESSION   I12881
VERSION     I12881.1  GI:910858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2470)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Assays for agonists and antagonists of recombinant human calcium
            channels
  JOURNAL   Patent: US 5429921-A 14 04-JUL-1995;
FEATURES             Location/Qualifiers
     source          1. .2470
                     /organism="unknown"
BASE COUNT      483 a    722 c    754 g    511 t
ORIGIN


  Query Match            84.0%;  Score 16.8;  DB 5;  Length 2470;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | ||||
Db    509 TCCATGACGTTCCAGCCGTT 490


RESULT  11
I12880/c
LOCUS       I12880       5467 bp    DNA             PAT       26-JUL-1995
DEFINITION  Sequence 12 from patent US 5429921.
ACCESSION   I12880
VERSION     I12880.1  GI:910857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5467)
  AUTHORS   Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
            and Brenner,R.
  TITLE     Assays for agonists and antagonists of recombinant human calcium
            channels
  JOURNAL   Patent: US 5429921-A 12 04-JUL-1995;
FEATURES             Location/Qualifiers
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RESULT   3
AB016662S3/c
LOCUS       AB016662S3    595 bp    DNA             ROD       14-APR-2000
DEFINITION  Mus musculus gene for aldose reductase, exon 9.
ACCESSION   AB016664
VERSION     AB016664.1  GI:4586467
KEYWORDS    aldose reductase.
SEGMENT     3 of 4
SOURCE      Mus musculus (strain:BALB/c) DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Li,H., Nobukuni,Y., Gui,T. and Yabe-Nishimura,C.
  TITLE     Characterization of genomic regions directing the cell-specific
            expression of the mouse aldose reductase gene
  JOURNAL   Biochem. Biophys. Res. Commun. 255 (3), 759-764 (1999)
  MEDLINE   99160426
REFERENCE   2  (bases 1 to 595)
  AUTHORS   Yabe-Nishimura,C. and Li,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1998) to the DDBJ/EMBL/GenBank databases. Chihiro
            Yabe-Nishimura, Kyoto Prefectural University of Medicine,
            Department of Pharmacology; Kawaramachi-Hirokoji, Kamikyoku, Kyoto,
            Kyoto 602-8566, Japan (E-mail:nchihiro@basic.kpu-m.ac.jp,
            Tel:+81-75-251-5333, Fax:+81-75-251-5348)
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
     exon            276. .358
                     /number=9
                     /product="aldose reductase"
BASE COUNT      133 a    161 c    151 g    150 t
ORIGIN


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  Best Local Similarity   94.7%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ccatgacgttcctgacgtt 20
          |||||||||||| ||||||
Db    215 CCATGACGTTCCAGACGTT 197


RESULT   4
A89782
LOCUS       A89782         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 4 from Patent WO9832462.
ACCESSION   A89782
VERSION     A89782.1  GI:6738296
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B. and Heeg,K.
  TITLE     PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
            OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
  JOURNAL   Patent: WO 9832462-A 30-JUL-1998;
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | ||
Db      1 TCCATGACGTTCCTGATGCT 20


RESULT   5
A89783
LOCUS       A89783         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 5 from Patent WO9832462.
ACCESSION   A89783
VERSION     A89783.1  GI:6738297
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipford,G.B. and Heeg,K.
  TITLE     PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
            OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
  JOURNAL   Patent: WO 9832462-A 30-JUL-1998;
            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          |||||||||||||||| | ||
Db      1 TCCATGACGTTCCTGATGCT 20


RESULT   6
A90869
LOCUS       A90869         20 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 4 from Patent EP0855184.
ACCESSION   A90869
VERSION     A90869.1  GI:6739263
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      6 c      4 g      7 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 5;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
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Db      1 TCCATGACGTTCCTGATGCT 20
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c	13	16.8	84.0	7175	5	AR022380	AR022380 Sequence
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c	15	16.8	84.0	7175	5	AR067883	AR067883 Sequence
c	16	16.8	84.0	7177	67	HUMCACHNTA	M94173 Human N-typ
c	17	16.8	84.0	7362	5	AR022379	AR022379 Sequence
c	18	16.8	84.0	7362	5	AR063882	AR063882 Sequence
c	19	16.8	84.0	7362	5	AR067882	AR067882 Sequence
c	20	16.8	84.0	7364	67	HUMCACHNT	M94172 Human N-typ
c	21	16.8	84.0	7713	3	RABBCCBIII	D14157 Rabbit mRNA
c	22	16.8	84.0	30713	32	CELW05G11	AF040660 Caenorhab
c	23	16.8	84.0	69051	83	AC073171	AC073171 Homo sapi
c	24	16.8	84.0	124595	90	HSJ322E17	AL109937 Homo sapi
	25	16.8	84.0	148871	78	AC025324	AC025324 Homo sapi
	26	16.8	84.0	170595	78	AC025937	AC025937 Homo sapi
c	27	16.8	84.0	186526	69	AC008669	AC008669 Homo sapi
c	28	16.4	82.0	3694	12	AF224508	AF224508 Mus muscu
	29	16	80.0	2271	7	AF135189	AF135189 Arabidops
	30	16	80.0	82686	7	AC004669	AC004669 Arabidops
	31	16	80.0	133137	10	AC007245	AC007245 Homo sapi
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	33	15.8	79.0	615	81	AC048760	AC048760 Giardia i
c	34	15.8	79.0	720	8	CNS01CTC	AL115960 Botrytis
	35	15.8	79.0	758	85	AC076687	AC076687 Giardia i
c	36	15.8	79.0	762	81	AC051209	AC051209 Giardia i
	37	15.8	79.0	768	81	AC055639	AC055639 Giardia i
c	38	15.8	79.0	777	84	AC075866	AC075866 Giardia i
c	39	15.8	79.0	790	80	AC037305	AC037305 Giardia i
c	40	15.8	79.0	799	81	AC058159	AC058159 Giardia i
	41	15.8	79.0	823	80	AC039484	AC039484 Giardia i
	42	15.8	79.0	873	81	AC049019	AC049019 Giardia i
	43	15.8	79.0	1084	81	AC048024	AC048024 Giardia i
	44	15.8	79.0	1195	81	AC050023	AC050023 Giardia i
	45	15.8	79.0	1551	8	ERGGEGH7A	L40638 Blumeria gr

ALIGNMENTS

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RESULT   1
AF053408
LOCUS       AF053408     4227 bp    DNA   circular  SYN       17-OCT-1998
DEFINITION  Expression vector pMCG16-S, complete sequence.
ACCESSION   AF053408
VERSION     AF053408.1  GI:3746485
KEYWORDS    .
SOURCE      Expression vector pMCG16-S.
  ORGANISM  Expression vector pMCG16-S
            artificial sequence; vectors.
REFERENCE   1  (bases 1 to 4227)
  AUTHORS   Krieg,A.M., Wu,T., Weeratna,R., Efler,S.M., Love-Homan,L., Yang,L.,
            Yi,A.K., Short,D. and Davis,H.L.
  TITLE     Sequence motifs in adenoviral DNA block immune activation by
            stimulatory CpG motifs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12631-12636 (1998)
  MEDLINE   98445422
REFERENCE   2  (bases 1 to 4227)
  AUTHORS   Wu,T., Efler,S.M., Davis,H.L., Krieg,A.M. and Schorr,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-1998) HGD, Loeb Health Research Institute, 725
            Parkdale Ave., Ottawa, ON K1Y 4E9, Canada
FEATURES             Location/Qualifiers
     source          1. .4227
                     /organism="Expression vector pMCG16-S"
                     /db_xref="taxon:82306"
     gene            3528. .4208
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     CDS             3528. .4208
                     /gene="S"
                     /note="derived from Hepatitis B virus surface antigen"
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                     /transl_table=11
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                     /protein_id="AAC64341.1"
                     /db_xref="GI:3746486"
                     /translation="MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGG
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                     FLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPFLPLLPI
                     FFCLWVYI"
BASE COUNT     1021 a   1076 c    990 g   1140 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 13;  Length 4227;
  Best Local Similarity  100.0%;  Pred. No. 4.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db   2444 TCCATGACGTTCCTGACGTT 2463


RESULT   2
AF053409
LOCUS       AF053409     4625 bp    DNA   circular  SYN       17-OCT-1998
DEFINITION  Expression vector pMCG50-S, complete sequence.
ACCESSION   AF053409
VERSION     AF053409.1  GI:3746487
KEYWORDS    .
SOURCE      Expression vector pMCG50-S.
  ORGANISM  Expression vector pMCG50-S
            artificial sequence; vectors.
REFERENCE   1  (bases 1 to 4625)
  AUTHORS   Krieg,A.M., Wu,T., Weeratna,R., Efler,S.M., Love-Homan,L., Yang,L.,
            Yi,A.K., Short,D. and Davis,H.L.
  TITLE     Sequence motifs in adenoviral DNA block immune activation by
            stimulatory CpG motifs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12631-12636 (1998)
  MEDLINE   98445422
REFERENCE   2  (bases 1 to 4625)
  AUTHORS   Wu,T., Efler,S.M., Davis,H.L., Krieg,A.M. and Schorr,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-1998) HGD, Loeb Health Research Institute, 725
            Parkdale Ave., Ottawa, ON K1Y 4E9, Canada
FEATURES             Location/Qualifiers
     source          1. .4625
                     /organism="Expression vector pMCG50-S"
                     /db_xref="taxon:82307"
     gene            3926. .4606
                     /gene="S"
     CDS             3926. .4606
                     /gene="S"
                     /note="derived from Hepatitis B virus surface antigen"
                     /codon_start=1
                     /transl_table=11
                     /product="surface antigen subtype ayw"
                     /protein_id="AAC64342.1"
                     /db_xref="GI:3746488"
                     /translation="MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGG
                     TTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG
                     MLPVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGK
                     FLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPFLPLLPI
                     FFCLWVYI"
BASE COUNT     1084 a   1193 c   1082 g   1266 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 13;  Length 4625;
  Best Local Similarity  100.0%;  Pred. No. 4.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatgacgttcctgacgtt 20
          ||||||||||||||||||||
Db   2444 TCCATGACGTTCCTGACGTT 2463
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 4, 2000, 20:47:25 ; Search time 993.06 Seconds
(without alignments)
87.962 Million cell updates/sec

Title: US-09-369-941-2
Perfect score: 20
Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_prl:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: gb_ba3:*
31: gb_in1:*
32: gb_in2:*
33: gb_in3:*
34: gb_pl3:*
35: gb_pr4:*
36: em_ba1:*
37: em_ba2:*
38: em_htg1:*
39: em_htg2:*
40: em_htg3:*
41: em_htg4:*
42: em_htg5:*
43: em_htg6:*
44: em_htg7:*
45: em_htg8:*
46: em_htg9:*
47: em_htg10:*
48: em_htg11:*
49: em_htg12:*
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52: em_htg15:*
53: em_htg16:*
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55: em_htg18:*
56: em_htg19:*
57: em_htg20:*
58: em_htg21:*
59: em_htg22:*
60: em_htg23:*
61: em_hum3:*
62: em_hum4:*
63: em_hum5:*
64: em_hum6:*
65: gb_pr5:*
66: gb_pr6:*
67: gb_pr7:*
68: gb_htg1:*
69: gb_htg2:*
70: gb_htg3:*
71: gb_htg4:*
72: gb_htg5:*
73: gb_htg6:*
74: gb_htg7:*
75: gb_htg8:*
76: gb_htg9:*
77: gb_htg10:*
78: gb_htg11:*
79: gb_htg12:*
80: gb_htg13:*
81: gb_htg14:*
82: gb_htg15:*
83: gb_htg16:*
84: gb_htg17:*
85: gb_htg18:*
86: gb_htg19:*
87: gb_htg20:*
88: gb_htg21:*
89: gb_htg22:*
90: gb_htg23:*
91: gb_sts1:*
92: gb_sts2:*
93: gb_vi1:*
94: gb_vi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	4227	13	AF053408	AF053408 Expressio
	2	20	100.0	4625	13	AF053409	AF053409 Expressio
c	3	17.4	87.0	595	12	AB016662S3	AB016664 Mus muscu
	4	16.8	84.0	20	5	A89782	A89782 Sequence 4
	5	16.8	84.0	20	5	A89783	A89783 Sequence 5
	6	16.8	84.0	20	5	A90869	A90869 Sequence 4
	7	16.8	84.0	20	5	A90870	A90870 Sequence 5
	8	16.8	84.0	20	5	A93512	A93512 Sequence 5
	9	16.8	84.0	20	5	A93521	A93521 Sequence 14
c	10	16.8	84.0	2470	5	I12881	I12881 Sequence 14
c	11	16.8	84.0	5467	5	I12880	I12880 Sequence 12
c	12	16.8	84.0	7113	33	D86600	D86600 Loligo blee